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AAX33810 standard; DNA; 1776 BP.
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                                                                                                   October 7, 2005, 17:30:12; Search time 919 Seconds (without alignments) 11440.109 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aax33810 Coding se	Aaz65072 Membrane-	Aac91561 Human PRO	Aas21472 Human cDN	Aas46225 Human DNA	Aaf44218 Human PRO	Abl88154 Human PRO	Ab195643 Human ang	Aca89675 cDNA enco	Aca73685 Human sec	Aca06000 Human sec	Aca66834 cDNA enco	Aca64371 Novel hum	Acf20409 Human sec	Acf19795 Human sec	Acd22083 Human sec	Acf13248 Human sec	Acd25351 Human sec	Acf00400 Human sec	Aca57998 cDNA enco
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ALIGNMENTS

This sequence encodes a human secreted protein of the invention. The secreted proteins were obtained from human adult placentar foctal brain, adult testes or adult blood cDNA libraries. The polymorleotides (PNB) and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions Secreted protein, human, nutritional activity; cytokine; tissue growth, cell proliferation; cell differentiation; immune stimulant; chemotaxis; immune suppressant; haematopoiesis regulator; activin; inhibin; cadherin; chemokinesis; haemostasis; thrombolysis; anti-inflammatory; gene therapy; tumour invasion suppressor; tumour inhibitor; ss. Merberg D; Evans C, New polynucleotides encoding secreted human proteins. Coding sequence for human secreted protein bn97_1. Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Treacy M, Agostino MJ, Spaulding V; Claim 1; Page 78; 96pp; English. 98WO-US018724. 97US-00929007 (GEMY) GENETICS INST INC. WPI; 1999-229235/19. P-PSDB; AAY05317 WO9913066-A1. Homo sapiens 08-SEP-1998; 08-SEP-1997; 18-MAR-1999.

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1681 CAGTTCCTATTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATA 1740
  AAGGTGACTGACTGCCCTCTGCAACTACAATAGCAGAGTGAGCCAGGCGGTGCCAAAG
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in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemokinetic activity, haematopoiesis and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The PNs are also stated to be useful for gene therapy
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 Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;
pharmaceutical; receptor immunoadhesin; gene mapping; ss.
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                                                                                                                                                                  The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIB ligands and various enzymes. The membrane-bound proteins and receptor immunoadhesins, for instance, can be used as therapeutic agents receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by recombinant techniques
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Yuan J;
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Wood WI,
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antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as meuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and inflammatory, angiogenic and immunological disorders
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                                                   CAGTICCTATTITCTICCATIGACCCATATTIATACCTTICAGGTACTGAAGATTTAATA
 CTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTT
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Watanabe CK,
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99WO-US030999.
2000WO-US000376.
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15-MAR-2000; 2000WO-US006884.
30-MAR-2000; 2000WO-US008439.
17-MAY-2000; 2000WO-US013705.
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P-PSDB; AAB50959.
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                         AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAG
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Human cDNA sequence encoding for PRO1131 polypeptide

(first entry)

24-OCT-2001

XEXEXEX

AAS21472;

BP

AAS21472 standard; cDNA; 1841

AAS21472

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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; probtate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS21244-AAS21518 encode for novel human secretory and transmembrane polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing P
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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99WO-US028634.
99WO-US028551.
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99WO-US028565.
99WO-US030095.
99WO-US03099.
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2000WO-US003565.
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1 ME, Goddard S
Stewart TA,
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P-PSDB; AAU12400.
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22-MAY-2000; 2
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16-DEC-1999;
20-DEC-1999;
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breakt, prostate, rectal, cervical or liver tumours by comparing PRO breakt, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour differentiation of chondrooytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells of T- lymphocytes, the proliferation of the PRO in portion of inner ear utricular supporting cells of T- lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor (VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymclecides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy
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Matches 1765; Conserv
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primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, casts, cattle, horses, sheep, pigs, goats and rebbits but are prefet by human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also breast, prostate, rectal, cervical, or liver tumours in mammalian subjects. The oligomucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
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Pred. No. 0;
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                                                                                                                                             PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss; dog; cat; pig; goat; rabblt; tumour necroesis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
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ttanabe CK, Wood WI, Zhang Z;
                                                                                                          Human DNA encoding PRO polypeptide sequence #301
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AAS46225 standard; cDNA; 1841
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The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bioactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide
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                       AAF44218 standard; cDNA; 1841
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                                               AAF44218;
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 CTTCTGAACTGTTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGG
                                                              CAAGGCCTAGTTGAGACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTGACT
             AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAG
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Wood WI;
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                                                                                PRO; cytostatic;
tissue typing;
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ID NO:318
sequence SEQ
                                                                                protein; I
                                                                                Human; secreted and transmembrane cancer; chromosomal mapping; gene
Human PRO1131 (UNQ569) nucleotide
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99US-0141037P.
99US-0144758P.
99US-0145698P.
99US-0145622P.
99WO-US021090.
99WO-US021547.
99WO-US021847.
99WO-US028313.
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P-PSDB; AAB65251.
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28-JUL-1999;
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and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 the AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65136 to AAB65300 represent human PRO polynucleotide and protein sequences given
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                                                     the exemplification of the present invention
                                                                                                DB
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Pred. No. 0;
0; Mismatches
                                                                                               99.3%;
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1765, Conservative
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Best Local S:
Matches 1765
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1215 1200 1335 1320 1455 1440 1575 1680 1380 1500 1620 1755 Human, angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAG GTTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCCATCTGTCCA TGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA **AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAG** CAAGGGCTAGTTGAGACATTGGGAATGGAACATAATCAGGAAAGACTATCTCTGACT AGTACAAAATGGGTTCTCGTGTTTCCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTT ACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTTTTCTTCTCAA TGTCTAATATCACCTCCCTGTTTTCATGTCTTCCTTACACTTGGTGGAATAAGAAACTTT TGCCGTTTCCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA GCATTCCTTCCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTC CTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTT CAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATA CAAGGGCTAGTTGAGACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACT TGTCTAATATCACCTCCCTGTTTTCATGTCTTCCTTACACTTGGTGGAATAAGAAACTTT TTGAAGTAGAAGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATC AGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTTTTGTTT AGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAATACACAAGGAATTCTTTTTGTTT GTTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGTCCA CCAGGAAAGAAATATATCCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCC CCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCC CTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTT CAGTTCCTATTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATA TTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCT sequence SEQ ID NO:165 1766 ATAATAAATGTAAATACTGTGAAAAA BP. standard; cDNA; 1841 (first entry) Human PRO1131 cDNA 16-MAY-2002 ABL88154 XX AC ABL88154; XX AC ABL88154; XX I 16-MAY-200 XX I WAY-200 XX Human PRO1 XX KW Human; ang 1216 1336 1576 1696 1816 1021 1096 1156 1141 1276 1261 1396 1516 1561 916 1036 1081 1201 1321 1381 1456 1441 1636 1681 1756 1741 1621 901 196 1501 RESULT ద 쉱 ò 셤 g ò g g ð g 셤 g 셤 8 g g 셤 g 셤 ò 8 ð ò ò ઠ δ Š õ 8

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gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
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Williams PM, Wood WI,
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2000WS-0222695P.
2000WS-0232522.
2000WS-0233528.
2000WS-0230978P.
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JF, Watanabe CK,
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atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polymucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                           196 CCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGCGCA
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gene therapy; endothelial disorder;
hypotensive; vulnerary;
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1, Hillan KJ, Marsters SA,
1X, Williams PM, Wood WI,
 atherosclerosis; cardiac hypertrophy; cardiant; cytostatic; antiangiogenic; antiarteriosclerotic; gene; ss.
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2000US-0220624P.
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Godowski PJ, Gurney A'
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MARSTERS S A.
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PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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P-PSDB; ABB95505.
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                                                            CAAGGGCTAGTTGAGACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACT
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                                                 The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosting a cardiovascular, endothelyl angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention
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 useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
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                                                                                                                                             Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;
                              Claim 1; Fig 165; 567pp; English.
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Matches 1765, Conservative
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 Human; PRO polypeptide; secreted protein; transmembrane protein; chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical; liver; cancer; TNF-alpha; tumour necrosis factor-alpha; proliferation; differentiation; chondrocyte cell; bone disorder; cartilage disorder; sports injury; arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
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                                                                                   Homo sapiens.
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                                                           1516 TGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAAATGCCTTATAAA
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                                                                                           GCATTCCTGCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTC
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01-MAR-2000;
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17-MAY-2000;
22-MAY-2000;
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18-SEP-2000;
18-SEP-2000;
18-FEB-2000;
18-FEB-2000;
22-FEB-2000;
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02-JUN-2000;
28-JUL-2000;
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28-FEB-2001;
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01-JUN-2001;
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06-AUG-2001;
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Gurney AL; , Goddard A, Godowski PJ, Wood WI, Zhang Z; Desnoyers L, Smith V, Watanabe CK, Chen J. 8 Pan J, Baker

WPI; 2003-332034/31. P-PSDB; ABU86493.

Three hundred and five nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, and for detecting the presence of tumor in a mammal.

Claim 2; Fig 601; 707pp; English.

The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane), sequences 80% identical to them, or encoding a PRO polypeptide lacking its associated signal peptide or an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide. Also included are the encoded PRO proteins, PRO expression vectors, host cells transformed with the vector (used to produce PRO proteins), a chimaeric molecule comprising the PRO antibody, a method for stimulating the release of tumor necrosis factor alpha (TMR-alpha) from human blood (by contecting the blood with PRO1979, PRO91), PRO131, PRO1316, PRO1183, PRO1343, PRO1357, or PRO43331, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the PRO6229 polypeptide,

·7a method for detecting the presence of tumour in a mammal and an algonucleotide probe derived from any of the nucleotide sequences cited above. The PRO polypeptide or anti-PRO antibody is useful for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in a binding reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful for detecting the presence of a tumour in a mammal, stimulating proliferation or differentiation of chondrocyte cells, stimulating the release of tumour necrosis factor-alpha from human blood, in gene cherapy, or as molecular weight markers for protein electrophoresis. purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. The present sequence is a cDNA encoding a PRO The protein 8888888888888888888888888888888888

Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

ö 540 135 120 180 255 240 315 300 375 360 435 420 495 480 555 615 900 675 9 735 720 9 76 AGCTCACAGTAGCCCGGCGGCCCAGGGCAATCCGACCACATTTCACTCTCACTGTAG GAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATGGGGACA GAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGACATGCTGGATGATGATGGGGACA CCACCATGAGCCTGCATCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGGCGCA AAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGGAGTCTGCATGTGG CTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTA AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTTTTTGGA 1 AGCTCACAGTAGCCCGGCGGCCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAG ccaccangagccrecarrercaagccrereccacaacregecarecagagceeegga CAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGACTTTGT GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTTGTTTTTTCAGTACTACCAGC **AAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG** CTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGCGCCCTTGTA CAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTT CAGAACAATGGAAATGGCATGGAACAATTGCTACCAGTTCTATAAAGACAGCAAAAAGTT AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTTCTACTCTTATTGGA Gaps Score 1764.4; DB 8; Length 1841; Pred. No. 0; 0; Mismatches 1; Indels 0; 99.3%; 99.9%; Query Match Best Local Similarity 99.9 Matches 1765; Conservative 61 136 121 196 256 241 316 301 376 361 436 421 496 481 541 919 601 919 661 181 ઠે 심 ò g δ g δ 셤 ઠે g ઠે 셤 Š 셤 ò g ઠે g ઠ g ઠે g ò

1095 1155 1395 1035 1516 TGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCCTATAA 1575 900 975 960 840 CTTCTGAACTGTTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAAGCAGAGACTGTGG AAGGTGACTGATTCGCCCTCTGCAACTACAATAGCAGAGTGAGCCAGGCGGTGCCAAAG CAAGGGCTAGTTGAGACATTGGGAAAATGGAACATAATCAGGAAAGACTATCTCTGACT TTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATC TTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATC GCATTCCTTCCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTC 1576 GCATTCCTTCCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTC AGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCG 916 AGAGAAGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCG 1096 AGTACAAAATGGGTTCTCGTGTTTCCTGTTCAGGATCACCAGCATTCTGAGCTTGGGGTT ACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTTCTTCAA TGTCTAATATCACCTCCCTGTTTTCATGTCTTCCTTACACTTGGTGGAATAAGAAACTTT CCAGGAAAGAAATATACCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCC CCAGGAAAGAAATATCCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCC CAAGGGCTAGTTGAGACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACT AGTACAAAATGGGTTCTCGTGTTTCCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTT TGECTAATATCACCTCCCTGTTTTCATGTCTTCCTTACACTTGGTGGAATAAGAAACTTT 1396 AGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTTTTTGTTT GTTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGTCCA TGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAAATCTCAATGCCTTATAA CTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTT CAGTTCCTATTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATA CAGTICCTATTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATA AGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTTTTGTTT 1841 ATAATAAATGTAAATACTGTGAAAAA 1766 901 1156 1141 1216 1276 1336 1321 1681 1816 964 781 856 841 916 1036 1021 1201 1261 1381 1441 1561 1636 1621 1696 1756 736 721 961 1081 1501 1741 à ò ઠે 셤 ò 셤 ઠ 셤 ઠે ď Š g ò q 셤 ò 셤 ठ 셤 8 ద ઠે 셤 ઠ g ઠે 셤 g ઠે g Š 요 ð- 원 ò g Š

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Baker KP,
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                                                                 Human, gene, ss, secreted and transmembrane protein, PRO, TNP-alpha,
tumour necrosis factor alpha, chondrocyte cell, tumour, gene therapy;
                                                      Human secreted/transmembrane protein (PRO) cDNA #301.
                     ACA06000 standard; cDNA; 1841 BP
                                                                                                                                                                                                                            99WO-USO20111.
99WO-USO21090.
99US-00403297.
99US-00423844.
99WO-USO28301.
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99US-00380138.
99US-00380139.
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2000WO-US005601.
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10-MAY-2001; 2001US-00854208.
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98US-00187368
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                                           (first entry)
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05-JAN-2000;
18-FEB-2000;
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                                                                            tissue typing
                                                                                        Homo sapiens.
                                                                                                                         12-JUL-2002;
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02-JUN-2000;
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01-DEC-1999;
02-DEC-1999;
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06-NOV-1998
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                                ACA06000;
          RESULT 11
ACA06000
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The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the proliferation or differentiation of chondroyte cells by contacting the cells with a PRO polypeptide, a method for detecting the presence of a tumour in a mammal and an oligonuclectide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for simulating the proliferation or differentiation of chondrocytes and effecting the presence of a tumour. The PRO polypeptides and nucleic acids may also be used diagnostically for tissue typing. The sequences presented in ACAAOS/700-ACAOGO04 are the cDNAs encoding the PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gurney AL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen J, Desnoyers L, Goddard A, Godo
ith V, Watanabe CK, Wood WI, Zhang Z;
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2001MO-US019692.
2001MO-US021066.
2001MO-US021735.
2001US-00908827.
2001US-00918585.
2001US-009294419.
                                                                                                                                                                                                                                                                                  16 AUG-2001; 2001US-00931836.
28-AUG-2001; 2001US-00941992.
29-AUG-2001; 2001WO-US027099.
04-SEP-2001; 2001US-00946374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JAN-2002; 2002US-00052586
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18-JUL-2001;
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            20-JUN-2001;
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255 240 315

T; 0 U; 0 Other;

490

C; 387 G;

512 A; 452

BP;

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Goddard A, Godowski PJ, Gurney AL;
ood WI, Zhang Z;
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Watanabe CK, Wood WI,
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                                                       99WO-US031274.
2000WO-US00219.
2000WO-US004341.
2000WO-US004414.
2000WO-US005004.
2000WO-US005004.
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2000WO-US023328.
2000US-00664610.
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2001WO-US006520.
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2001US-00854208
2001US-00854280
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2001WO-US021735.
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09-JUL-2001;
18-JUL-2001;
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30-MAY-2000;
28-JUL-2000;
28-JUL-2000;
24-AUG-2000;
18-SEP-2000;
18-SEP-2000;
08-NOV-2000;
08-NOV-2000;
01-DEC-2000;
20-DEC-2000;
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25-MAY-2001;
01-JUN-2001;
05-JUN-2001;
20-JUN-2001;
12-NOV-1999;
01-DEC-1999;
02-DEC-1999;
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10-MAY-2001;
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Pan J,
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Three hundred and five nucleic acids encoding secreted and transmembrane PRO polypeptides, useful for the diagnosis, prevention and/or treatment of tumors, such as adrenal, lung, colon, breast, prostate, rectal,

The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane). Methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of tumours, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumours. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence represents a cDNA encoding a human PRO polypeptide of the invention

1020 ö 135 195 180 240 315 300 375 360 435 420 495 480 555 540 615 9 675 999 735 720 795 780 855 840 915 900 975 960 9 CCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGCCCA CAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGCTGCTGACTTTGT CTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTA CTGAAAAACTCTGTCGTGGTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTA CAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTT CTTCTGAACTGTTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGG AGAGAAGGCCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCG AGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCCCTGAAACATAGGCG AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAG CAAGGCTAGTTGAGACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACT GAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGACATGCTGGATGATGAGGGACA CCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGCGCA GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCCTTTTTGTTTTTTCAGTACTACCAGC TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAGAAGATTAGGAAATACGTCCC AAGAGTTGCAATCTCTACAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGGATGTGG CAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTT AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGA AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGA cadederririocececerdacaderescandescrierescrieresariosaridaaececerrica CTTCTGAACTGTTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGG CCATCCTTAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTG 1 AGCTCACAGTAGCCCGGCCCCAGGCCAATCCGACCATTTCACTCTCACCGCTGTAG CAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGTTTGT Gaps ; 0 Length 1841; Indels 8 ; 8 Score 1764.4; Pred. No. 0; 0; Mismatches 99.3**%**; 99.9**%**; Best Local Similarity 99.9 Matches 1765, Conservative Sequence 1841 9/ 196 256 316 376 919 919 964 856 841 901 961 19 121 241 361 436 421 929 541 601 199 736 721 916 916 Query Match 181 301 496 481 781 ద 셤 g a q 셤 ò 셤 ਨੇ g ठ 셤 ઠ 임 ઠે 셤 ð 셤 è 셤 ઠે B ઠે 셤 ò g ઠે 8 δ ò ઠે ò

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New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
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                               2000WO-US005004
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The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA, 209439, 201315, etc); or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide. The PRO polypeptides or polynuclectides are useful as pharmaceuticals, diagnostics, biosensors or biorector. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma, leukaemia or lymphoma), hepstitis B, multiple sclerosts, or Crohn's disease in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases.

The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA.

The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a novel human secreted and transmembrane PRO polypeptide

Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

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ö 9 1 AGCTCACAGTAGCCCCGGCGCCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAG Gaps , 0 Indels 1, Pred. No. 0; 0; Mismatches Query Match Best Local Similarity 99.9 Matches 1765; Conservative

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                                                                          1276 TGTCTPATATCACCTCCCTGTTTTCATGTCTTCCTTACACTTGGTGGAATAAGAAACTTT
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98US-01010683P.
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98US-0100619P.
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Human; PRO; secreted protein, transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy; gene; ss.
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RR 23-SEP-1998 PBUS-01011472P.

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RR 23-SEP-1998 PBUS-0101

Query Match 99.3%; Score 1764.4; DB 8; Length 1841; Best Local Similarity 99.3%; Pred. No. 0; Matches 1765; Conservative 0; Mismatches 1; Indels 0; Gaps

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1776)

S Jacobs,K., Mccoy,J.M., Lavallie,E.R., Racie,L.A., Evans,C., Merberg,D., Treacy,M., Agostino,M.J. and Spaulding,V.

S Secreted proteins and polynucleotide encoding the same secreted proteins and polynucleotide encoding the same

L Patent: JP 2001515717-A 1 25-SEP-2001;

GENETICS INSTITUTE INC
OS Homo sapiens (human)

PN JP 2001515717-A/1

PD 25-SEP-2001

PF 08-SEP-1999 UP 2000510854

PR 08-SEP-1997 US 08/929007

PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI
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ò	241 GCTTGGTGCTGCTGATAGGGCTGGGGGGCCTTTTGTTTTTTCAGTACTACCAGC 300			AGAAATTGG
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à	781 CCATCCTTAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTG 840		ACCESSION ARE	AR528680 AR528680.1
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à	901 AAGGTGACTGATTGGCCCTCTGCAACTACAAATAGCAGAGGTGAGCCAGGCGGTGCCAAAG 960			Crane test
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Patent: WO 0168848-A 601 20-SEP-2001;
Genentech, Inc. (US)
Location/Qualifiers
1. .1841 1841 bp I Sequence 601 from Patent WO0168848. AX376534 AX376534.1 GI:19170655 1261 1441 1621 1681 DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS RESULT 5 AX376534 LOCUS JOURNAL TITLE FEATURES . QQ 요 ò ନ୍ଧ 8 셤 ઠે g ò ઠે g δ 요 ઠે g ઠે g ઠે 셤 8 셤 ò g ઠ 셤

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Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnoyers, L., Eaton, D. Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K.,
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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PRINTING BURNING: Burker, K. P. Perrara, N. Gantata, Cranitata, Vertebrate, Butchoentoni, Burker, K. P. Perrara, N. Gather, E. Gararhini, Hemindes, Panin, C. Perrara, Burning: Burker, K. P. Perrara, N. Gather, E. Gararhini, Hemindes, Panin, J. Perrara, Burning, E. Stephan, J. P. Watcher, E. C. Strillame, K. B. Gadard, A. Codada, H. L. Gadorati, P. J. Stephan, J. P. Watcher, E. C. Strillame, P. W. Wood, W. I. Burning, E. Stephan, J. P. Watcher, E. C. Williame, P. W. Wood, W. I. Candon, E. C. Stephan, J. P. Watcher, E. C. Williame, P. W. Wood, W. I. Burning, E. Stephan, J. P. Watcher, E. C. Williame, P. W. Wood, W. I. Burning, E. Construction, C. Construction, E. C. Williame, P. W. Wood, W. I. E. D. Hillan, Remark J. (193) Jane, Real P. (193) Perrara, Napoleone Andrey (EDS) Paning, M. Construction, E. C. Williame, P. Watcher, E. Godard, March (EDS) Construction, C. (193) Perrara, Construction, C. (193) Const		1021 AGTACAAATGGGTTCTCGTGTTTCCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTT 1080	
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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1200 1275 1440 1500 TIGAAGTAGAAGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATC 1395 1755 780 840 900 975 960 720 795 855 AGAGAAGGCCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCG CTTCTGAACTGTTCCATATTATAATAGTGTCACCAGCCCAAGAAGCAGAGACTGTGTGG CTTCTGAACTGTTCCATATTATAATAGATGTCACCAGCCCAAGAAGAAGAAGAGCAGTCTGTGTGG AAGGTGACTGACTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAG 1036 CAAGGGCTAGTTGAGACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACT AGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTTTTGTTT TGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA GCATTCCTTCCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTC AGAGAAGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCG CAAGGGCTAGTTGAGAAATGGAAACATAATCAGGAAAGACTATCTCTCTGACT TTGAAGTAGAGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATC AGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTTTGTTT GTTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCCATCTGCCTTGTCCA TGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA 1576 GCATTCCTTCCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTC AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTATTGGA

	61 AGAMGACCIGAMITICOCOGGICAGAGCIACICIGAGITITICACICICITITICAL 62 AAGAMGACCICAMITICOCOCCICAGAGCIACICAGAGTITICACICICITICICAL 73 CAGAGCITITOGACCCCAAAAATATATAAAAAAAAAAAAAAAAAAAAAA	
Qy 1681 CAGTTCCTATTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTTAATA 1740 Db	PAY 191058 AX491058 REGION Sequence 165 from Patent W00200590. REGION AX491058 Homo sepiens REGION R	Qy 481 CAGAACAATGGGAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTT 540

300 375 360 435 420 495 480 555 540 615 9 675 9 735 720 795 780 855 840

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136 GAATCCAGATGCCAGAGGCCAGGAGCAGCAGGAGGACATGCTGGATGATGATGGTGGGGACA
                                                                                                                                                               CCACCATGACTCTCAAGCCTCTGCCAAACTCGGCATCCAAGCCCCGGGCGCAA
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                                     76 AGCTCACAGTAGCCCGGCGCGCGAATCCGACCACATTCACTCTCACCCGCTGTAG
                                                                                                                                          CCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGGCA
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                                                                        GAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGACATGCTGGATGATGATGGGGACA
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I (bases 1 to 1841)

I (bases 1 to 1841)

Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Gimmaldi, C., Gu,Q., Hass, P.B., Heldens, S., Huang, A., Kim, H.S., Kilmowski, L., Jün, Y., Johnson, S., Elee, J., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagte, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Kie, M.H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W.I. and Godowski, P., The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins:
                                                                      1755
                                                                                                     CAGTICCTATITICTICCATIGACCATATITATACCTITICAGGIACTGAAGAITIAATA 1740
                                                                                                                          1756 CAGTICCTATTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATA 1815
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LQVQNIKLAGSLQHVARKLCRELYNKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWED
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SELFHIIIDVTSPRSRDCVAILNGMIPSKDCKELKRCVCERRAGMVKPBSLHVPPFTT
GEGD"
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 CCAGGAAAGAAATATATCCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCC
                                   CTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTT
                                                     CTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTT
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Homo sapiens clone DNA59777 QAKY569 (UNQ569) mRNA,
AY358587
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Genome Res. 13 (10), 2265-2270 (2003)
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FLI CDNA.
Homo sapiens (human)
Homo sapiens
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Clark, H.F.
Direct Submission
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Matches 1765, Conservative
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 168 Row: k Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23503320.
Location/Qualifiers
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterffield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Geheration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 943
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                              Strausberg, R. Direct Submission Submits of Health, Mammalian Submitted (19-MAR-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 ACAGTAGCCCGGCCCCAGGCAATCCGACCAATTTCACTCTCACCGCTGTAGGAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-romail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael Brownstein / Ted Usdin
                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/lab host="DH108"
/note="Vector: pBluescript"
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/db_xref="taxon:9606"
/clone="MGC:87010 IMAGE:30337675"
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/db_xref="LocusID:51267"
/db_xref="MIM:606782"
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/gene="CLEC1"
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Best Local Similarity 100.
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E. (bases 1 to 2701)

Straubberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Butchow, R.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsich, F., Diatchenko, L., Marusina, K. Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Pithyk, S.W., Worley, K.J., Male, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
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1 ACAGTAGCCCGGCCCAGGGCAATCCGACCACTTTCACTCTCACCGCTGTAGGAATC 60 66 CAGATGCAGGCCAAGTACAGCAGGACATCCGATTTCACTCTCACCGCTGTAGGAATC 60 66 CAGATGCAGGCCAAGTACAGCAGCAGGACATGCTGGATGATGATGGGACACCCC 120 61 CAGATGCAGGCCAAGTACAGCAGCAGGACATGCTGGATGATGATGAGGACACCACC 120 62 ATGAGCCTGCATTCTCAAGCCTCTGCCACACTCGGCATCCAGAGCCCCGGCGCACAGAG 185 63 ATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGGGGCACAGAG 180 64 ATGAGCCTGCATTCTCAAGCCTTGCACACTGGCATGACTTTGTGCTTG 245 65 ATGAGCCTCCTCTTCAAGCTGGCAACCAGTGGCCTGACCTTGCTTG	GTGCTGCTGATAGGGCTGCCCGGGGCTTTTGTTTTTCAGTACTACCAGCTCTCC	421 AAACTCTGTCGTGGGCCGTGTATAACAAGCTGGAGGGGGGGG	606 GACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTTATTGGACAGGG 665	126 GAACTGTTCCATATTATAATAGATGTCACCAGCAGAGAGCAGAGACTGTGTGGCCCATC 785	906 GACTGATTCGCCCTCTGCAACTACAATAGCAGAGGCCAGGCCGCAAAGCAAGG 965
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                                                        ATGECTICCTTACACTIGGIGGAATAAGAAACTITITGAA 1265
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Imates, Catarrhini, Hominidae, Homo.
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T., Nagai,K., Kojima,S., Otsuki,T. and
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Primer for synthesizing full-length CDNA and use thereof.
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       GACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGACCAGGCGGTGCCAAAGCAAGG
                                    GACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGG
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07-JUL-2000
JP 200253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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PD 22-03M-2002
PD 22-03M-2000
PD 2002017375-A/2934
PD 07-JUL-2000
PD 2002017375-A/2934
PI TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUN PI ISHII,
PI YURI KAWAI,AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NACAI, PI SHINCHI KOJIWA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC CIZNIS/09, CO7K14/47, C07K16/18, C12NI/15, C12NI/19, C12NI/21, C12NS/ 1
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                        C C12P21/02,C1201/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00
Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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Location/Qualifiers
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/db_xref="G1:22760992"
/db_xref="G1:2276099
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                                                                                                                                                                                                                                                                                                            AK075114 1756 bp mRNA linear PRI 03-SEP-2002 Homo sapiens cDNA FLJ90633 fis, clone PLACE1003573, weakly similar to T-CELL SURFACE GLYCOPROTEIN YE1/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAGATGCAGGCCAAGTACAGCAGGACACGAGGACATGCTGGATGATGATGAGGGGACACCACC 125
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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fissue type="pLacenta"
/clone lib="PLACE1"
/note="cloning vector: pME18SFL3"
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/note="unnamed protein product"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/product="C-type lectin-like receptor-1"
/protein id="AAH39072.1"
/brotein id="AAH39072.1"
/db_xref="G1:24660226"
/db_xref="Iocus 12.124660226"
/db_xref="Iocus 12.1257"
/db_xref="MIM:606782"
/db_xre
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SELFHIIIDVTSPRSRDCVAILNGMIPSKDCKELKRCVCERRAGMVKPESLHVPPETL
GEGD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 51 Row: o Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7706062.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GCCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAGGAATCCAGATGCAGGCCAA 60
                                                                                                                                                                                                                                                                                                                       Submitted (01-NOV-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/clone lib="NIH MGC_115"
/lab_host="DH10B"
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing Center Conter code: BCM-HGSC Center code: BCM-HGSC Center http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, I.Kowis, C.R., Sheed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAGGAATCCAGATGCAGGCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Pregator: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="MGC:34328 IMAGE:5178017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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Pred. No. 0;
0; Mismatches
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/db_xref="LocusID:51267"
/db_xref="MIM:606782"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/codon_start=1
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Matches 1756;
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AUTHORS
TITLE
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                                                       TITLE
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                                                                                                       Strausberg, R.L., Feingold, B.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schenfer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Younghan, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
                                                                                                                                                                   1260
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           1141 TAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTTTTCTCAATGTCT 1200
                                                                                                                                                                                                                                               GTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAA 1325
                                                                                                                                                                                                                                                                                                                       1261 GTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGTGACAGTCAAGTAGTCCATCAGAAA 1320
                                                                                                                                                                                                                                                                                                                                                                                                       1385
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1797)
                                                                                                                                   1201 AATATCACCTCCCTGTTTTCATGTCTTCCTTACACTTGGTGGAATAAGAAACTTTTTGAA
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92.4%;
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STRANDEDNESS: single
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; CLONE: 1355922
US-09-055-095-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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Best Local Similarity
 TOPOLOGY: line
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                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                          STATE: C. COUNTRY:
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2, Appli
                                                                  October 7, 2005, 19:54:21; Search time 329 Seconds (without alignments) 8832.910 Million cell updates/sec
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Sequence 1
Sequence 8
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Sequence 3
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                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-460-84A-194
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US-09-113-789-2
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US-09-113-789-2
US-09-113-788-2
                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                 1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                                OM nucleic - nucleic search, using sw model
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                                                                                                         US-10-689-742-159
1776
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Maximum DB seq length: 2000000000
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1114 TTTACATGCCACCAACCTAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAG 1083 TTTACATGCCACCAACCACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAG 1174 ATAACTTTAGCTCTTTCTTCTCAATGTCTAATATCACCTCCTGTTTTCATGTCTTC 1143 ATAACTTTTAGCTCTTTTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCATGTCTTC 1234 CTTACACTTGGTGGAATAAGAAACTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCT 1203 CTTACACTTGGTGGAATAAGAAACTTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCC 1203 CTTACACTTGGTGGAATAAGAAACTTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCC	Oy 1294 TTTCTCTGACAGTAGTAGTCATCGAGAATTGGCAGTCCTCCCAGATTGTACCAG 1353	Qy 1474 AGAATCTCAAATCTCAATGCTTATAAGCATTCCTTCCTGTGTCCATTAAGACTCTCATA 1533 HIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	Oy 1654 CCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCATTGCCATTTTA 1713	RESULT 2 US-09-643-597-194 Sequence 194, Application US/09643597 Sequence 194, Application US/09643597 GENERAL INFORMATION: APPLICANT: Wang, Tongtong APPLICANT: Ralos, Michael D. APPLICANT: Ralos, Michael D. APPLICANT: Bangur, Chaitanya S. APPLICANT: Hosken, Nancy APPLICANT: Fanger, Gary R. APPLICANT: Hosken, Nancy APPLICANT: Wang, Ailun APPLICANT: Wang, Ailun APPLICANT: Wang, Ailun APPLICANT: Skeiky, Yasir A.W.	APPLICANT: Henderson, Robert A. APPLICANT: McNeill, Patricia D. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.455C11 CURRENT APPLICATION NUMBER: US/09/643,597 CURRENT PILING DATE: 2000-08-21 NUMBER OF SEQ ID NOS: 369 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 194 LENGTH: 320 TYPE: DNA TYPE: DNA CRANISM: Homo sapiens
Conservative		CABAG CABAG CABAG TTGCT TTGCT TGBAA	SAGCT SAGCT SAGCT SGCCT SGCCT		ÀCATTAGGGGAAGGTGACTGATTCGCCCC GGTGCCAAAGCAAGGGCTAGTTGAGACACA GGTGCCAAAGCAAGGGCTAGTTGAGACACA CTCTCTGACTAGTACAAAATGGGTTCTCC [
Matches 1694; Conservative Qy 76 CCAAGTACAGCAGCACG Db 3 CCAAGTACAGCAGCACGCACG Qy 136 ATTCTCAAGCTCTCGC Db 63 ATTCTCAAGCTCCGGCC Qy 196 CCTCTTCAACGTGGCGA Qy 123 CCTCTTCAACGTGGCGA Db 123 CCTCTTCAACGTGGCGA	9 6 6 6 7 6	3 9 9 4 3 6 3 4 4 5 4 5 4 6 9 4 6 9 4 6 9 4 6 9 9 6 9 9 9 9 9 9	574 P 574 P 5 634 P 5 634 P 634 P 63 P 603	Oy 694 GGCTGTGGATGGATGGAACCC Db 663 GGCTGTGGATGGATGGAACCC Qy 754 CCAGCCCAAGAAGCAAGACC Ob 723 CCAGCCCAAGAAGCAAGACC Oy 814 GCAAAGAATTGAAGCTTGT Db 783 GCAAAGAATTGAAGCGTTGT OY 874 TCCATGTCCCCCTGAAACA	Db 843 TCCATGTCCCCCTGAA Oy 934 AGCAGAGTGACCAGGO Db 903 AGCAGATTGAGCCAGGO Qy 994 TAATCAGGAAAGACTAT Db 963 TAATCAGGAAAGACTAT Oy 1054 GATCACCAGCATTCTG Db 1023 GATCACCAGCATTTTTG Db 1023 GATCACCAGCATTTTTG Db 1023 GATCACCAGCATTTTTG

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CCAGAAAAAAGIGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCC 1698
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Pred. No. 3.9e-90;
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Sequence 194, Application US/09542615A

Patent No. 6518265

GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Ralos, Michael D.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Hosken, Nancy A.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CAN; FILE REFERENCE: 210121.455C8
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: US/09/542,615A
CURRENT APPLICATION NUMBER: 100-04-14

NUMBER OF SEQ ID NOS: 350

SOFTWARE: FRESENCE: 320

SEQ ID NO 194

SEQ ID NO 194

LENGTH: 320
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7 100.0%; Pred. No. 5.-
... 0; Mismatches
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Patent No. 6531315
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Ran, Chaitanya S.
APPLICANT: Hosken, Mancy Nancy
                                                                                                       1699 ATTGACCCATATTTATACCT 1718
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Best Local Similarity 100.
Matches 320; Conservative
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; ORGANISM: Homo sapiens
US-09-542-615A-194
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                                         Length 320;
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18.0%; Score 320; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 3.9e-90;
Matches 320; Conservative 0; Mismatches 0; Indels
                                                                                   0; Indels
                                                                                                                           1399 CCCTTCCCAATCCATCAGTAAAGACCCCCATCTGCCTTGTCCATGCCGT
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Patent No. 6482597
GENERAL INFORMATION:

APPLICANT: Wang, Tongtong
APPLICANT: Hosken, Nancy A.

APPLICANT: Allow, Michael D.

APPLICANT: APLICANTON: COMPOUNDS AND METHODS FOR THERAPY

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121-455C6

CURRENT APPLICATION NUMBER: US/09/480, 884A

CURRENT FILING DATE: 2001-08-27

NUMBER OF SEQ ID NOS: 330

SEQ ID NO 194

LENGTH: 320
                                       18.0%; Score 320; DB 3; 100.0%; Pred. No. 3.9e-90; ive 0; Mismatches 0;
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                                   Query Match
Best Local Similarity 100.
Matches 320; Conservative
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; ORGANISM: Homo sapiens
US-09-480-884A-194
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                                                                                                                                                                                                                                                                                                             1459 ATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAAGCATTCCTTTCCTGTGTCC
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Patent No. 6696247

GENERAL INFORMATION:

APPLICANT: WANG: COMPOUNDS AND METHODS FOR THERAPY AND TITLE OF INVENTION:

PILE REPERENCE: 210121.455C4

CURRENT APPLICATION UNMER: US/09/466,396A

CURRENT FILING DATE: 1999-12-17

NUMBER OF SEQ ID NOS: 224

SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 320
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C9
CURRENT APPLICATION NUMBER: 2000-06-28
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FactSEQ for Windows Version 3.0
SEQ ID NO 194
LENGTH: 320
                                                                                                                                                                                                                               Length 320;
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                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                            18.0%; Score 320; DB 4; I
100.0%; Pred. No. 3.9e-90;
tive 0; Mismatches 0;
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llarity 100.0%; Pred. No. 3.9e-90;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 320; Conservative
                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-09-466-396A-194
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320; Conserv
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US-09-466-396A-194
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1638 1458 1578 ö CCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGA 1638 61 ATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAAGCATTCCTTCTGTGTCC 120 241 CCAGAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCC 300 241 CCAGAAAAAGTGAGCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCC 300 9 181 CCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGA CCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCC CCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGA 1 CCCTTCCCATCATCAGTAAAGACCCCCATCTGCCTTGTCCATCGCGTTTCCCAACAGGG 181 CCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAGAGAGTTAAAGA CCAGAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTCC 1399 CCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGG ATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAAGCATTCCTTGTGTCC Gaps ; 0 Length 320 0; Indels APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Ranger, Gary R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY OF
TITLE OF INVENTION: LUNG CANCER
FILE REFERENCE: 210121.45555
CURRENT APPLICATION NUMBER: US/09/476,496A
CURRENT FILING DATE: 1999-12-30 Query Match
18.0%; Score 320; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 3.9e-90;
Matches 320; Conservative 0; Mismatches 0; NUMBER OF SEQ ID NOS: 254 SOFTWARE: FastSEQ for Windows Version 3.0 Sequence 194, Application US/09476496A ; Patent No. 6706262 ; GENERAL INFORMATION: 1699 ATTGACCCATATTTATACCT 1718 ATTGACCCATATTTATACCT TYPE: DNA
CORGANISM: Homo sapiens
US-09-476-496A-194

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SOFTWARE: Patent.pm
SRQ ID NO 8301
LENGTH: 162
TYPE: DNA
ORGANISM: Homo sapie
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STRANDEDNESS:
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BEREIN No. 6783961

GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Dunclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.022.RG
CURRENT FILMG DATE: 2000-02-24
PRIOR PAPLICATION NUMBER: US 60/122,487
PRIOR PAPLICATION NUMBER: US 60/122,487
PRIOR PAPLICATION NUMBER: US 60/122,487
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                                                                                                                                                                                                                                                                   APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121,455C10
CURRENT APPLICATION NUMBER: US/09/630,940B
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 367
SOPTHARE: PRETERO for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 320;
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Pred. No. 3.9e-90;
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18.0%; Score 320; DE
Best Local Similarity 100.0%; Pred. No. 3.9
Matches 320; Conservative 0; Mismatches
                   Sequence 194, Application US/09630940B Patent No. 6737514
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                                                        GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Pan, Liqun
APPLICANT: Ralos, Wichael D.
APPLICANT: Hosken, Nancy
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aijun
                                                                                                                                                                                                                                                      Skeiky, Yasir A.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
CORGANISM: Homo sapiens
US-09-630-940B-194
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  US-09-630-940B-194
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LENGTH: 320
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46 AGCTCACAGTAGCCCGGCGGCCCAGGCAATCCGACCACATTCACTCTCACCTCTAG 105
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                                                                                                           1 AGCTCACAGTAGCCCGGCGCGCACAATCCGACCACATTTCACTCTCTCACCGCTGTAG 60
                                                                                                                                                                                                               61 GAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGACATGCTGGATGATGATGGGG 117
                                                                                                                                                                                                                                                106 GAATCCAGATGCAGGCCAAGTACAGCAGCAGCAGGACATGCTGGATGATGATGGGGG 162
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                                                       Gaps
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  Length 162;
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4.7%; Score 82.6; DB 1; Length 9
Best Local Similarity 58.2%; Pred. No. 5.3e-15;
Matches 145; Conservative 0; Mismatches 104; Indels
                                                       0; Indels
                                                                                                                                                                                                                                           US-08-690-095-2
; Sequence 2, Application US/08690095
; Sequence 2, Application US/08690095
; Patent No. 5792648
; GENERAL INFORMATION:
; APPLICANT: Hullman, Jennifer L.
; APPLICANT: Au-Young, Janice
; TITLE OF INFORMATION: NOVEL HUMAN MACROPHAGE ANTIGEN
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
ZIP:
Score 117; DB 4; I
Pred. No. 2.2e-26;
  Query Match
6.6%; Score 117; DB
Best Local Similarity 100.0%; Pred. No. 2.2
Matches 117; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAMME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF-0110 US
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 970 base pairs
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503 ATATAGCAAAGAACAAGAGCACAAATGTAAGCCTTGTCCAAGGAGATGGATTGGCATAA 562
                                                                                                                           563 gcacaccierrarrecraagrearcarcraacarccaacarccaccaccaccacaraaarcccrc 622
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                                                                  503 AGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTG
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58.2%; Pred. No. 5.3e-15;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION NUMBER: US/09/016,434
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 800, Application US/09016434
| Patent No. 650038
| GENERAL INPORMATION:
| APPLICANT: Janice Au-Young APPLICANT: Janice Au-Young APPLICANT: Janice Norman Composition For INVENTION: PATHWAY GENE EXPRESSION NUMBER OF SEQUENCES: 1490
| CORRESPONDENCE ADDRESS: ADDRESSE: STREET: 3174 PORTER DRIVE CITY: PALO ALTO
| STATE: CALIFORNIA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 104;
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REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
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TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 8
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nucleic acid
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Matches 145; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        623 GTCTCAGAG 631
                                                                                                                                                                                                                                                                                                                                                                                        683 ATCCCAGAG 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPHGNOT03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
US-09-016-434-800
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503 ATATAGCAAAGAACAAGAGACAAAATGTAAGCCTTGTCCAAGGAGATGGATTTGGCATAA 562
                                                                                                                                                         563 GGACAGCTGTTATTTCCTAAGTGATGATGTCCAAACATGGCAGGAGGTAAAATGGCCTG 622
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58.2%; Pred. No. 5.3e-15;
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Patent No. 6034219
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
OPERATING SYSTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,789
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
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REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-01
TELECOMMUNICATION INFORMATION:
TELEFAM: 415-845-055
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 145, Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                      GTCTCAGAG 631
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CLONE: 513418
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                                   503 AGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTG 562
                                                                                                        495 CAAGATCAGGAACCTCTCCACCACACTGCAAACAATAGCCACCAAATTATGTCGTGAGCT 554
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503 ATATAGCAAAGAACAAGAGCACAAATGTAAGCCTTGTCCAAGGAGATGGATTTGGCATAA 562
                                                                                                                                            623 TGCTGCTCAGAATGCCAGCCTGTTGAAGATAAACAACAAAATGCATTGGAATTTATAAA 682
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                                                                   563 GEACAGCTGTTATTTCCTAAGTGATGATGTCCAAACATGGCAGGAGAGTAAAATGGCCTG
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Pred. No. 8e-15;
0; Mismatches 104; Indels
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US-09-48-273-34

Sequence 34, Application US/09482273

Sequence 34, Application US/09482273

Sequence 34, Application US/09482273

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT PILING DATE: 1090-01-13

CURRENT PILING DATE: 2000-01-13

EARLIER PILING DATE: 1999-07-14

EARLIER PILING DATE: 1998-07-15

SEARLIER PILING DATE: 1998-07-15

NUMBER OF SEQ ID NOS: 267

SEQ ID NOS: 267

SEQ ID NOS: 267

LENGTH: 1737
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; OTHER INFORMATION: n equals a,t,g, or
US-09-482-273-34
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Best Local Similarity 58.2%;
Matches 145; Conservative
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735 ATCCCAGAG 743
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683 ATCCCAGAG 691
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FEATURE:
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NAME/KEY: SITE
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LOCATION: (167
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Sequence 1045, Application US/09976594

Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Burchinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2000-10-12
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SEQ ID NO 1045
LENGTH: 505
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   367 GATTTTCTTATGTCACAGCCATTACTCATGTTTTCGTTC---TTTTGGGCGGGATTATCA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGTGAGCTGTATAACAAAGCTGGAGCACACACAGGTGCAGCCCTTGTACAGAACAATGGAAA 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 caggaraactrarcccaggaactggggagcaacrccaacaactrgrccarggaggaggagrrr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
3.8%; Score 67.8; DB 4; Length 5:
Best Local Similarity 50.3%; Pred. No. 1.5e-10;
Matches 218; Conservative 0; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6673549 406707.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c, g, or other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAPPLICANT: Au-Young, Janice APPLICANT: Cocks, Benjamin G. APPLICANT: Goli, Surya K.
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LOCATION: 459, 463
CTHER INFORMATION: a, t,
US-09-976-594-1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens
  US-09-976-594-1045
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US-08:688-342-2
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468 IGCAGCCCTTGTACAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAA 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      708 GGAACCCCTTTCACTTCTGAACTGTTCCATATTATA 744
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APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCES ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRANCEO Version 1.5
SURRENT APPLICATION NUMBER: US/08/680,342
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 86,749
REFERENCE/DOCKET NUMBER: 86,749
REFERENCE/DOCKET NUMBER: 86,749
REFERENCE/DOCKET NUMBER: 18,749
RODE/OGY: LINEAR

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Run on:

Searched:

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Result

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
US-09-991-073-318
US-09-991-103-318
US-09-991-103-318
US-09-991-103-318
US-09-991-103-318
US-09-992-598-318
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ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 159, Application US/09746783

Publication No. US20030044935A1

GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

MCCOY, John M.

LaVallie, Edward R.

Racie, Lisa A.

Treacy, Maurice

Spaulding, Vikki

Agostino, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: WA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                             Description
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/cgm2 6/ptodata/2/pubpna/USO6 NEW PUB.seq:*

/cgm2 6/ptodata/2/pubpna/USO6 NEW PUB.seq:*

/cgm2 6/ptodata/2/pubpna/USO6 PUBCOMB.seq:*

/cgm2 6/ptodata/2/pubpna/USO8 PUBCOMB.seq:*

/cgm2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*

/cgm2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*

/cgm2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*

/cgm2 6/ptodata/2/pubpna/USO8 PUBCOMB.seq:*

/cgm2 6/ptodata/2/pubpna/USO8 NEW PUB.seq:*

/cgm2 6/ptodata/2/p
                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-989-723-318
US-09-989-279-318
US-09-989-727-318
US-09-989-731-318
US-09-989-731-318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     8443130 segs, 3482420727 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                      US-10-689-742-159
1776
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published
                                                                                                                                                                           October
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
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                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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Sequence 3 Sequence 3 Sequence 3

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1621 CTTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCCCTTCATCATCTGCACCTGTAATAGTTT
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                                                                                AGAGAAGGGCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCG
                                                                                                                             AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAG
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                                     CCATCCTTAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTG
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SEQUENCE DESCRIPTION: SEQ ID NO: 159:
US-09-746-783-159
                                                                                                                                                                                                                                   ВВ
                                                                                                                                                                                                                                  ; Score 1776; D; Pred. No. 0; 0; Mismatches
  APPLICATION NUMBER: US/09/746,783
                                                                                                                                                              TOPOLOGY: linear _ MOLECULE TYPE: other nucleic acid
            FILING DATE: 21-Dec-2000
CLASSIFICATION: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELECOMMUNICATION INFORMATION:
                                                                            TELEPHONE: (617) 227-7400
TELEPAX: (617) 227-7400
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
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                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.
Matches 1776; Conservative
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PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR PLING DATE: 1998-06-05
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PRIOR PLING DATE: 1998-06-05
PRIOR PPLING DATE: 1998-06-05
PRIOR PLING DATE: 1998-06-09
PRIOR PLING DATE: 1998-06-09
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PRIOR PLING DATE: 1998-06-11
PRIOR PLING DATE: 1998-06-11
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PRIOR PLING DATE: 1998-06-11
PRIOR PLING DATE: 1998-06-12
PRIOR PLING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/08953
PRIOR PLING DATE: 1998-06-17

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PRIOR PILING DATE: 1998-06-19
PRIOR FILING DATE: 1998-06-19
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PRIOR PILING DATE: 1998-06-19
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PRIOR PILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349
FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/090355
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1663
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CURRENT PELLING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PELLING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR PELLORION NUMBER: 60/065186
PRIOR PELLORION NUMBER: 60/065181
PRIOR PELLORION NUMBER: 60/065111
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PRIOR PELLORION NUMBER: 60/06970
PRIOR PELLORION NUMBER: 60/07910
PRIOR PELLORION NUMBER: 60/08910
PRIOR APPLICATION NUMBER: 60/089759
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PRIOR APPLICATION NUMBER: 60/089021
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R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088029
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/088030
R FILING DATE: 1998-06-04
                                               Sequence 318, Application US/09989722
Patent No. US20020072067A1
GENERAL INPORMATION:
APPLICANT: Ashkenazi,Avi J.
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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Napier, Mary A.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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: Williams, P. Mickey
: Wood, William I.
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Eaton, Dan L.
Ferrara, Napoleone
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Gerber, Hanspeter
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Botstein, David
        US-09-989-722-318
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	376 TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGATTAGGAAATACGTCCC 435 361 AAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGGAAGTTGCAGGAAGTTGCAGGAAGTTGCAGGAAGTTGCAGGAAGTTGCAGGAAGTTGCAGGAAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG 495	421 CTGAAAAACTCTGTCGTCAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTA 480	CGGAGCACTGTAAATGCCAGCTGGGGCAATTGCTACCAGTTCTATAAGACAGCAAAGTT GCGAGCACTGTAAATGTTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAACAAACTT GCGAGCACTGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAAC	AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGA	735 CHOSSCIIIIGCGCCCIGALAGISSCAGGCCIGGGGGAGGGGGGGCCCIIILA 753 721 CTTCTGAACTGTTCCATATATAATAGATGTCACCAGGCCCAAGAAGCAGAGACTGTGTGG 780 796 CTTCTGAACTGTTCCATATTATAATAGATGTCACCAGACAGA	781 CCATCCTTAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGAAGGGTTGTGTCTGTG 840 	841 AGAGAAGGGAAGAAIGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCG 900	ANGETICACTICACTCTCTCTCTACTACTACTCTCTCTACTCTCTCT	961 CAAGGGTAGTTGAGACATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACT 1020 	1021 AGTACAAAATGGGTTCTCGTGTTTCCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTT 1080	1081 TATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGCCACCAACCA	1141 ACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGCTCTCTTTCTCAA 1200	1201 TGTCTAATATCACCTCCCTGTTTTCATGTCTTCCTTACACTTGGTGGAATAAGAAACTTT 1260	1261 TIGAAGTAGAGAAATACATIGAGGTAACATCCTTTTCTCTGACAGGTCAAGTAGTCCATC 1320
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1997-11-14
PRIOR PLING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/078910
PRIOR APPLICATION NUMBER: 60/08132
PRIOR APPLICATION NUMBER: 60/08132
PRIOR PLILING DATE: 1998-04-26
PRIOR PELLING DATE: 1998-04-26
PRIOR PELLING DATE: 1998-04-20
PRIOR PELLING DATE: 1998-05-29
PRIOR PELLING DATE: 1998-06-07
PRIOR APPLICATION NUMBER: 60/08102
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     1336 TTGAAGTAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATC 1395
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APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: William P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin I.
TITLE OF INVENTION: Secreted and Transmembran TITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
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Grimaldi, J.Christopher
Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
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Eaton, Dan I.
Ferrara, Napoleone
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Paoni, Nicholas F.
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Gerber, Hanspeter
Gerritsen, Mary E.
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Napier, Mary A.
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Botstein, David
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PRIOR FILING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PLING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR PILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/09166
PRIOR PELING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/09163
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Best Local Similarity 99.9%;
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PRIOR APPLICATION NUMBER: 60/08514
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PRIOR APPLICATION NUMBER: 60/08599
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PRIOR APPLICATION NUMBER: 60/08963
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99.3%; Score 1764.4;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-01
PRIOR PILING DATE: 1998-07-02
PRIOR FILING DATE: 1998-07-02
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PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
PRIOR PILING DATE: 1998-07-02
PRIOR PILING DATE: 1998-07-07
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NR APPLICATION NUMBER: 00/080505

R APPLICATION NUMBER: 60/088734

RR APPLICATION NUMBER: 60/088738

RR APPLICATION NUMBER: 60/088738

RR FILING DATE: 1998-06-10

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PRIOR PLING DATE: 1998-06-22
PRIOR PLING DATE: 1998-06-22
PRIOR PLLING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
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PRIOR PLLING DATE: 1998-06-32
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R APPLICATION NUMBER: 60/086212
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R APPLICATION NUMBER: 60/088655
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R FILING DATE: 1998-06-10
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088861
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088861
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-12
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FILING DATE: 1998-06-16
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FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
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LLING DATE: 1998-06-17
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19
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FILING DATE: 1998-06-23
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APPLICATION NUMBER: 60/088167
FILING DATE: 1998-06-05
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088326
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic CURRENT APPLICATION NUMBER: 108/049787
PRIOR APPLICATION NUMBER: 60/04250
PRIOR PELING DATE: 1997-06-16
PRIOR PELING DATE: 1997-06-11-12
PRIOR PELING DATE: 1997-06-11-13
PRIOR PELING DATE: 1997-06-11-24
PRIOR PELING DATE: 1997-06-25
PRIOR PELING DATE: 1998-06-25
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APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
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Gurney, Austin L.
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Paoni, Nicholas F.
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                                                                      APPLICANT: Ashkenazi, Avi J
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
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US20020103125A1
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PRIOR APPLICATION NUMBER: 60/065311 PRIOR PILING DATE: 1997-11-13 PRIOR PELICATION NUMBER: 60/066770 PRIOR PILING DATE: 1997-11-24 PRIOR PELICATION NUMBER: 60/0545 PRIOR PILING DATE: 1998-02-25 PRIOR PILING DATE: 1998-02-25 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-03-20 PRIOR PILING DATE: 1998-04-28 PRIOR PILING DATE: 1998-06-08 PRIOR PILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-28 PRIOR PILING DATE: 1998-05-28 PRIOR PILING DATE: 1998-05-28 PRIOR PILING DATE: 1998-06-02 PRIOR PILING DATE: 1998-06-02 PRIOR PILING DATE: 1998-06-02	PRIOR APPLICATION WUMBER: 60/087699 PRIOR FILING DATE: 1998-06-02 PRIOR PILING DATE: 1998-06-02 PRIOR FILING DATE: 1998-06-02 PRIOR PILING DATE: 1998-06-03 PRIOR APPLICATION NUMBER: 60/08021 PRIOR PILING DATE: 1998-06-04	##10# ##10#	FRICK APPLICATION UNMERS: 00/086801 FRICK PILING DATE: 1998-06-11 FRICK PILING DATE: 1998-06-11 FRICK PILING DATE: 1998-06-11 FRICK APPLICATION NUMBER: 60/089105 FRICK APPLICATION NUMBER: 60/089105 FRICK PILING DATE: 1998-06-12 FRICK PILING DATE: 1998-06-16
	1561 CCAGGAAATATTCCCCATCTCCGTTTCATATCGAACTACCGGTATTCT 162 1636 CCAGGAAACAATATTCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTC 162 1621 CTTCAGAAGAATATATCCCCATCTCCGTTTCATTCAGAACTACCGTCCCCGATATTC 169 1621 CTTCAGAAGAATATAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTT 168 1681 CAGTTCCTATTTATAAGACCAGAAAAAGTGAGCTCTTCATCTGCACCTGTAATAGTTT 175 1681 CAGTTCCTATTTCTTCCATTGACCCATATTAATACCTTTCAGGTACTGAAGATTTAATA 174 1756 CAGTTCCTATTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATA 174 1741 ATAATAAATGTAAATACTGTGAAAAA 1766 1816 ATAATAAATGTAAATACTGTGAAAAA 1841	9-732-318 ce 318, Application US/09989732 No. US22020123463A1 CANT: Ankenazi, Avi J. CANT: Baker, Kevin P. CANT: Buster, David CANT: Buster, David CANT: Betsen, Dan L. CANT: Ferrara, Napoleone CANT: Ferrara, Napoleone CANT: Gerber, Mary E. CANT: Gerber, Mary E. CANT: Grimandi, J. Christopher CANT: Grimaldi, J. Christopher CANT: Kljavin, Ivar J. CANT: Napier, Mary A. CANT: Roy, Margaret Ann CANT: Stewart, Timothy A. CANT: Stewart, Timothy A. CANT: Walliams, P. Mickey CANT: Walliam I. CANT: Walliam I. CANT: Walliam I. CANT: Zhang, Zemin	TITLE OF INVENTION: Sected and Iransmembrane Polypeptiques and Nucleic Although Acids Encoding the Same FILE REFERENCE: P2730PLC57 CURRENT PAPLICATION NUMBER: U5/09/989,732 CURRENT FILING DATE: 2001-11-19 PRIOR APPLICATION NUMBER: 60/049787 PRIOR PILING DATE: 1997-06-16 PRIOR PILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-10-17 PRIOR FILING DATE: 1997-11-12

1998-06-16 1998-06-17 1998-06-17 NUMBER: 60/089538 1998-06-17 NUMBER: 60/089598 1998-06-17 NUMBER: 60/089599 1998-06-17 NUMBER: 60/089509 1998-06-17 NUMBER: 60/089509	06-18 06-18 06-18 06-18 06-19 06-19 06-19 06-19 06-19 06-19 06-19 06-19 06-19 06-20 06	56/09054 56/09054 56/09054 56/09057 56/09067 56/09069 56/09069 56/09069 56/09069 56/09069 56/09086 56/09086 56/09086 56/09086 56/09086 56/09086 56/09086
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AGCTCACAGTAGCCCGGCGCGCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAG 135 136 GAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGGCGACA 195 CAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGGGCCCTGACCCTGCTGACTTGT 315 CCACCATGAGCCTGCATTCTCAAGCCTCTGCCAACTCGGCATCCAGAGCCCCGGCGCA GAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGACATGCTGGATGATGATGGGGGACA CCACCATGAGCCTGCATTCTCAAGCCTCTGCCACACTCGGCATCCAGAGCCCCGGCGCA CAGAGCACAGGGGTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT ö DB 9; Length 1841; 1; Indels Score 1764.4; Pred. No. 0; 0; Mismatches PRIOR APPLICATION NUMBER: 60/090431
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	Oy 1021 AGTACAAAATGGGTTTCCTGTTTCCTGTTCCAGGATCACCAGCATTTCTGAGGTT 1080	Db 1156 TATGCACGTATTTAACAGTCACAAGAAGTCTTATTACATGCCACCAACCTCAGAA 1215 Qy	Oy 1201 TGTCTAATATCACCTCCCTGTTTTCATGTCTTCCTTACACTTGGAATAAGAAACTTT 1260 1276 TGTCTAATATCACCTCCTGTTTTCATGTCTTCCTTACACTTGGTGGAATAAGAAACTTT 1335 Oy 1261 TTGAAGTAGAGGAAATACATTGAGGTAACATTCTTTCTGACGTGAATAAGAATTT 1335	1336 TICAAGTACAGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATC 139	Db 1396 AGAAATTGGCAGTCACTTCCCAGTTGTACCAGCAAATACCAAGGAATTCTTTTTGTTT 1455 Qy 1381 GTTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCGCCTTGTCCA 1440 Db 1456 GTTTCAGTTCATACTAGTCCCTTTCCCAATCAGTAAAGACCCCATCGCCTTGTCCA 1515	1441 TGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCCAAATCTCCAATGCCTTATAA 	Oy 1501 GCATTCCTTCTGTGTCCATTAAGACTCTGATAATTGTCTCCCTTCCATAGGAATTTCTC 1560	CCAGGAAAGAATATATCCCCATCTCCGTTTCATATCAGAACTACGGTCCCCGATATTCCCTTCAGAACTACTCGGTCCCCGATATTCCCTTCAGAAAAAAGAGAACTACCGTCTTCAGAACTACGAAAAAAAA	1696 CTTCAGAGAGATTAAAGACCAGAAAAAGTGAGCCTCTTCATCTGCACCTGTAATATTTTTTTT	1756 CAGTTCCTATTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATA 1741 ATAATAAATGTAAATACTGTGAAAA 1766 11816 ATAATAAATGTAAATACTGTGAAAA 1841	RESULT 10 US-09-991-163-318 ; Sequence 318, Application US/09991163 ; Patent No. US20020132253A1 ; GENERAL INFORMATION:
PRIOR FILING DATE: 1998-07-02 PRIOR APPLICATION NUMBER: 60/091544 PRIOR PILING DATE: 1998-07-01 PRIOR PILING DATE: 1998-07-02 PRIOR PILING DATE: 1998-07-02 PRIOR APPLICATION NUMBER: 60/091626 PRIOR APPLICATION NUMBER: 60/091632 PRIOR APPLICATION NUMBER: 60/091633 PRIOR FILING DATE: 1998-07-02 PRIOR PILING DATE: 1998-07-07 PRIOR PILING DATE: 1998-07-07 PRIOR PILING DATE: 1998-07-07 PRIOR PLING DATE: 1998-07-07 PRIOR PLING DATE: 1998-07-07 PRIOR PLING DATE: 1998-07-07 PRIOR FILING DATE: 1998-07-07 PRIOR FILING DATE: 1998-07-07	Query Match Best Local Matches 176		CCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCGGGGCA 18	181 CAGAGCACAGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT	Oy 241 GCTTGGTGCTGGTGGTGGCTGGGGCCTTTTTTTTGGTACTACTACTGGGGG 300 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Db 376 TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGATTAGGAAATACGTCCC 435 Qy 361 AAGAGTTGCAATCTCTTCAAGTCCGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG 420 Db 436 AAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG 495	Oy 421 CTGAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACAGGTGCAGCCTTGTA 480 	OY 481 CAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGT 540 	Qy 541 GGGAGGACTGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAAC	Qy 601 AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTTTTTGGA 660 Db 676 AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGA 735 Qy 661 CAGGGCTTTTGCGCCCTGACGCAGGCTGTGGATGGATGGA	Db 736 CAGGGCTTTTGCGCCCTGACAGTGGCAAGGCCTGTGGATGGA

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PRIOR APPLICATION NUMBER: 60/088167
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RPPLICANT: Zhang, Zemin
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Grimaldi,J.Christopher
Gurney,Austin L.
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Wood, William I.
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Stewart, Timothy A
Tumas, Daniel
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Fong, Sherman
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  Ashkenazi, Avi J.
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Eaton, Dan L.
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                                                                                1516 TCCCCTTTCCCCAACAGGGATGTCACTTGATATGAGAATCTCAAATCTCAATGCCTTATAA 1575
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                                                   GITTCAGTICATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGTCCA 1440
                                                                                                                                             1441 TGCCGTTTCCCAACAGGGATGTCACTTGATATGAGAATCTCAAAATCTCAATGCCTTATAA 1500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1741 ATAATAATGTAAATACTGTGAAAA 1766
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US-09-903-604-318
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Sequence 318, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi,Avi J.
APPLICANT: Baker,Kevin P.
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Grimaldi, J. Christopher
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Williams, P. Mickey
Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Gerritsen, Mary E.
Goddard, Audrey
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Botstein, David
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Eaton, Dan L.
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PRIOR PLICATION WUMBER: 60/08960

PRIOR FILING DATE: 1998-06-18

PRIOR PLICATION WUMBER: 60/08901

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255 300 360 435 675 855 840 135 195 180 240 315 420 495 480 555 540 615 900 099 735 720 795 780 9 AGCTCACAGTAGCCCGGCGGCGCGATCCGACCACTTTCACTCTCACCGCTGTAG 136 GAATCCAGATGCAGGCCAAGTACAGCAGGACGAGGGACATGCTGGATGATGATGGGGACA GCTTGGTGCTGCTGGTAGGGCTGGCAGCCCTGGGGCTTTTTGTTTTTCAGTACTACCAGC crgaaaaacrcrgrcgrgagcrgraraacaaagcrggagcacacaggrgcagcccrrgra CTICIGAACTGTICCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGG CTTCTGAACTGTTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGG AGCTCACAGTAGCCCGGGGGCCCAGGGCAATCCGACCATTTCACTCTCACCGCTGTAG GAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATGGGGACA CCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGCGCA CAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGACTTTGT CAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAGATTAGGAAATACGTCCC AAGAGTTGCAATCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG AAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAAGCTTGCAGGAAGTCTGCAGCATGTGG CTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTA CAGAACAATGGAAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTT CAGAACAATGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTT AAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGA Length 1841; ; 0 Indels 6 DB Score 1764.4; Pred. No. 0; 0; Mismatches PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
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PRIOR PLING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/09163
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PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091948
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R FILING DATE: 1998-06-24 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089410 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089948 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/089952 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089908 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 60/088202 APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/088858 FILING DATE: 1998-06-11 FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089105 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089532 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089538 FILING DATE: 1998-06-17 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-23 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 APPLICATION NUMBER: 60/089947 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 CATION NUMBER: 60/0 FILING DATE: 1998-06-16 FILING DATE: 1998-06-22 PRIOR PRIOR PRIOR

76 AGCTCACAGTAGCCCGGCGCCCAGGCAATCCGACCACTTTCACTCTCACCGCTGTAG 135 GCTTGGTGCTGCTGATAGGGCTGGCCAGCCCTGGGGCTTTTGTTTTTTCAGTACTACCAGC 300 CAGAGACAGGCCCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGCTGACTTTGT CCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGCGCA 196 CCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGCGCA CAGAGCACAGGGGTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT AGCTCACAGTAGCCCGGCGCCCAGGGCAATCCGACCACATTTCACTCTCACCGCTGTAG GAATCCAGATGCAGGCCAAGTACAGCACCACGAGGACATGCTGGATGATGATGGGGACA Gaps Length 1841; . 0 Indels DB 9; 1; Score 1764.4; Pred. No. 0; 0; Mismatches R APPLICATION NUMBER: 60/090535
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R APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/090472 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090862 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/090863 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-02 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 FILLING DATE: 1998-07-07 APPLICATION NUMBER: 60/092182 FILLING DATE: 1998-07-09 APPLICATION NUMBER: 60/090445 APPLICATION NUMBER: 60/091360 APPLICATION NUMBER: 60/090678 APPLICATION NUMBER: 60/091544 ; 0 99.3%; 1998-06-26 1998-06-24 FILING DATE: 1998-06-24 1998-07-03 Conservative Similarity FILING DATE: FILING DATE: FILING DATE: Matches 1765; 181 Н Query Match Best Local 61 121 256 241 PRIOR 1 PRIOR 셤 셤 셤 셤 Š ò Š ş à

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1381 GTTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGTCCA	00 1561 CCAGGAAAGAATATTCCCCATCTTCATATCAGAACTACCGCCCCCATTTC 1620 1636 CCAGGAAAGAATATTCCCCATTTCTTCTTCAGAACTACCGCCCCCCATTTCC 1636 CCAGGAAAGAATATTCCCCATTTCTTCAGACTACCGTCCCCGATATTCC 1695 1621 CTTCAGAGAATTAAAGACCAGAAAAAGTGAGACCTCTTCATCTGCACCTGTAATGTTT 1680 1696 CTTCAGAGAGATTAAAGACCAGAAAAAGTGAGACCTCTTCATCTGCACCTGTAATGTTT 1755 009 1681 CAGTTCCTATTTCTTCCATTGACCATTTATAACTTTCAGGTACTGAAGATTTAATA 1740 1756 CAGTTCCTATTTCTTCCATTGACCCATATTTATAACCTTTCAGGTACTGAAGATTTAATA 1815 009 1741 ATAATAAATGTAAAAA 1766 1816 ATAATAAATGTAAAAA 1841 1816 1816 ATAATAAATGTGAAAAA 1841	118-3 1-3 1-3 1-3 1-3 1-3 1-3 1-3 1-3 1-3 1	## APPLICANT: Godowski, Paul J. ## APPLICANT: Grimaldi, J.Christopher ## APPLICANT: Gurney, Austin L. ## APPLICANT: Kljavin, Ivar J. ## APPLICANT: Najarin, Ivar J. ## APPLICANT: Najarin, Mary A. ## APPLICANT: Pan, James ## APPLICANT: Pan, James ## APPLICANT: Pan, James ## APPLICANT: Pan, Margaret Ann ## APPLICANT: Tumas, Daniel ## APPLICANT: Tumas, Daniel ## APPLICANT: William P. Mickey ## APPLICANT: William P. Mickey ## APPLICANT: Applicant ## APPLICANT: Ap	; FILE REFRENCE: P2730P1C55 ; CURRENT APPLICATION NUMBER: US/09/989,721 ; CURRENT FILING DATE: 2001-11-19 ; PRIOR APPLICATION NUMBER: 60/049787 ; PRIOR PILING DATE: 1997-06-16 ; PRIOR PILING DATE: 1997-10-17 ; PRIOR PILING DATE: 1997-10-17 ; PRIOR PLING DATE: 1997-11-12 ; PRIOR APPLICATION NUMBER: 60/065311 ; PRIOR RELING DATE: 1997-11-13 ; PRIOR RILING DATE: 1997-11-13 ; PRIOR RILING DATE: 1997-11-13
375 360 435 420 495 495 555	540 615 600 675 735 720	780 855 840 915 900 975 960	1020 1095 1080 1155 1140 1215 1200	1260 1335 1320 1395 1380
316 GCTTGGTGCTGGTGAGGCCTGGGGCCTTTTGTTTTTTTTGAGTACTACCAGG 375 301 TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAGATTAGGAAATACGTCCC 360 316 TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAGATTAGGAAATACGTCCC 435 361 AAGAGTTGCAATCTTTCAAGTCCAGAATAAAAGCTTGCAGGAAGTTGCAGGAATACGTCCC 435 361 AAGAGTTGCAATCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG 420 436 AAGAGTTGCAATCTTCTTCAAGTCCAGAATAAAAAGCTTGCAGGAAGACTCTGCAGCATTTGTG 435 427 CTGAAAAAACTCTGTGAGGTGTATAACAAAGCTGGAGCACAAGGTGCAGCCCTTGTA 480 496 CTGAAAAAACTCTGTCGTGAGCTGTATAACAAAAGCTGGAGCACAAGGTGCAGCCCTTGTA 555	AGTT AAAC AAAC TTGGA TTGGA	721 CTTCTGAACTGTTCCATATTATAATAGTCACCAGGCCCAAGAAGCAGAACTGTGTGG 780 796 CTTCTGAACTGTTCCATATTATAATAGATGTCACCAGCCCAAGAACCAGAACTGTGTGG 855 781 CCATCCTTAATGGGATGATCTTCTCAAAGGACTGCAAGAACTTGAAGCTTGTGTTGTGG 840 856 CCATCCTCAATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTTTGTG 915 841 AGAGAAGGGCAGAATGGTGAAGCCAGAAGCATTGCCCCCTGAAACATTAAGCG 910 11	961 CAAGGCTAGTTGAGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACT 10 1021 AGTACAAAATGGCATTGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACT 10 1021 AGTACAAAATGGCTTCTGTGTTTCCTGTTCAGGATCACCAGCATTTCTGAGCTT 10 1096 AGTACAAAATGGGTTCTCGTGTTTCCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGTT 10 1091 TATGCACGTATTAAACAGTCACAAGAAGTCTTATTTACATGCCACCACCAACCA	1201 TGTCTAATATCACCTCCCTGTTTTCATGTCTTACACTTGGTGGAATAAGAACTTT 126

1997-11-24 NUMBER: 60/075945 1998-02-25 NUMBER: 60/078910 1998-03-20 1998-03-20 1998-04-28 NUMBER: 60/084600 11998-05-07 NUMBER: 60/084600 11998-05-07 NUMBER: 60/084600 11998-05-07 NUMBER: 60/08700 11998-05-07 11998-05-08		60/08874; 60/088874; 60/08881; 60/08882; 60/08885; 60/08885; 60/08885; 60/08885; 60/08886; 60/08887; 60/08887; 60/08887; 60/08887; 60/08887; 60/08887; 60/08887; 60/08981; 60/08981; 60/08953; 60/08953;
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1276 TGTCTAATATCACCTCCCCTGTTTTCATGTCTTCCTTACACTTGGTGGAATAAGAAACTTT 1335
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                                AGAGAAAGGCCAGGAATGGTGAAGCCAGAGACCTCCATGTCCCCCCTGAAACATTAGGCG
                                                                                AAGGTGACTGACTTGCCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCCGGTGCCAAAG
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                                                                   AAGGTGACTGATTCGCCCTCTGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAAG
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1756 CAGTICCTAITTICTICCAITGACCCATAITTATACCTITCAGGTACTGAAGAITTAAATA
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PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR PILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR PILING DATE: 1998-07-02
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Best Local Similarity 99.9%;
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PRIOR FILING DATE: 1998-06-05
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R APPLICATION NUMBER: 60/089952
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R APPLICATION NUMBER: 60/090246
R APPLICATION NUMBER: 60/090252
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PRIOR APPLICATION UNDER: 60/090429
PRIOR PILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
                         FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/088217
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FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/090355
FILING DATE: 1998-06-23
APPLICATION NUMBER: 60/088202
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CURRENT FILING DATE: 2001-11-14

PRIOR PAPLICATION NUMBER: 60/06250

PRIOR PAPLICATION NUMBER: 60/06251

PRIOR PAPLICATION NUMBER: 60/065311

PRIOR PAPLICATION NUMBER: 60/065311

PRIOR APPLICATION NUMBER: 60/065311

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PRIOR PAPLICATION NUMBER: 60/06311

PRIOR PAPLICATION NUMBER: 60/06310

PRIOR PAPLICATION NUMBER: 60/08322

PRIOR PAPLICATION NUMBER: 60/08106

PRIOR PAPLICATION NUMBER: 60/08022

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R RFILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/086033

R APPLICATION NUMBER: 60/08632

R APPLICATION NUMBER: 60/086326

R RILING DATE: 1998-06-04

R RILING DATE: 1998-06-04

R APPLICATION NUMBER: 60/088167

R RILING DATE: 1998-06-05
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Grimaldi, J.Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
Zhang, Zemin
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Stewart, Timothy A.
                                                                                         Ferrara, Napoleone
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Paoni, Nicholas F.
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Goddard, Audrey
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Botstein, David
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                                   Desnoyers, Luc
                                                                                                                      Fong, Sherman
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                                  376 TCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAGAGATTAGGAAATACGTCCC
                                                                                                AAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGG
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Najer, Nay A.
APPLICANT: Najer, Mary A.
APPLICANT: Pao, James
APPLICANT: Pao, James
APPLICANT: Pao, Margaret Ann
APPLICANT: Pao, Margaret Ann
APPLICANT: Pack Danie, Nicholas F.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: APPLICANT: Wood, Williams, P. Mickey
APPLICANT: APPLICATION NUMBER: 00049787
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065186
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   GITTCAGITCAIACTAGICCCTICCCAAICCAICAGIAAAGACCCCCAICIGCCTIGICCA 1440
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Ferrara, Napoleone
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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PRIOR PILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR FILING DATE: 1998-07-07
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR APPLICATION NUMBER: 60/09182
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 9100 GENYZ cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CKS91145 1734 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI049YB09 of Placenta Cot 25-normalized of fmon sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1734) Lid, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3X358767 BX358767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
                                                     BX365099 | BX351794 | BX106079 | BX106079 | BX349047 | BX349047 | BX349047 | BX340311 | CB992128 | CB992129 | CB992139 | CB997137 | 
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plasmid="pcMvSPORT_6"
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99.9%; Pred. No. 0;
ive 0; Mismatches
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/clone="CS0D1049YB09"
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/clone="CSODI041YA14"
/tissue_type="Placenta Cot 2!
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Pred. No. 0;
0; Mismatches
                                                               Query Match 95.2%;
Best Local Similarity 99.9%;
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CK614400 1671 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0D1036YF20 of Placenta Cot 25-normalized cof Homo sapiens (human).
                          CCATTAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTCCCAGGAAGAAATATA
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                                                  Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 9100 GENYX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 9100 GENYX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitogen.

Location/Qualifiers
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http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
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                                      Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
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/clone="CSOD1036YP20"
/tissue_type="placenta_Cot_25-normalized"
/plasmid="pCMVSPORT_6"
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                                   Eukaryota: Metazoa; Chordata; Craniata; Verte
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1 (bases 1 to 1671)
Li, M.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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larity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
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/organism="Homo sapiens"
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CR614400.1 GI:50495207
HTC; CNSLT_CDNA.
         HTC; CNSLT_CDNA.
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Homo sapiens
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348 GGAAATACGTCCCAAGAGTTGCAATCTTTCAAGTCCAGAATATAAAGCTTGCAGGAAGT 4 	408 CTGCAGCATGTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGG [528	588 AAGATAAACAAACAAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTTC	648	708 GGRACCCCTTTCACTTCTGAACTGTTCCATATTATAGATGTCACCACCCCAAGAAGCCCTTTCACTTCTGAACTGTTCCATATTATAATAGAATGTCACCAGCCCAAGAAGCATGTACAAAGGAACGATCTTCAAAAGAACTGTTAAAATAGAATGAAAAAAAA		841 888 901	948 GGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAATCAGGAAAGCC 1007 	1008 IAICICICIGACIAGIACAAAAIGGGIICICGIGIITICCIGIICAGGAICACCAGCAIIT 	1068	1141 ACCACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCCTTAGAGATAACTTTTAGCTCTTCTTGGCCTTAGAGATAACTTTTTAGCTCTTCTTGGTCTTACACTTTGGTGGTGTGTAGACTTTGGTCTTACACTTTGGTGGTGTGTTTTTTAGAGATAACACTTGGTGTTTTTTAGAGATAACACTTTGGTGGTGTGTTTTTTTT	1201 TCTTCTTCTACATGTCTAATATCACCTCCCTGTTTTCATGTCTTCCTTACACTTGGTGG	128 ANTAGARACITITIGARGIANAGANAIRACAIGACARACARACARACA COLITICION CONTROL CONTRO	1321 CAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGA	1368 ATTCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCTAGTCCTTCTTCTTTTTTTT
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Oy 1680 TCAGTICCTATITICTICCATIGACCCATATITATACCTITCAGGTACTGA 1730 	_		ENGATYOLA; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 1747) AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D. TITLE Full-length cDNA libraries and normalization		ALTERANCE 2 (Dates 1 to 1/4/) AUTHORS Genoscope TITLE Direct Submission JOURNAL Submitted (20-UUL-2004) Genoscope - Centre National de Sequencage : JOURNAL RP 191 91006 EVEY cedex - FRANCE (E-mail : serrefærencene ens fr	COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a	division of Invitrogen. FEATURES Location/Qualifiers source 1.1747 /mol_type="mRNA"	/db.xrer="texon:9606" /clone="C\$OD1067YX14" /tissue_type="Placenta Cot 25-normalized" /plasmid="pcMVSPORT_6"	Query Match Query Match Query Match 33.0%; Score 1651.4; DB 3; Length 1747; Matches 1704; Conservative 0; Mismatches 1; Indels 42; Gaps 1;	CATITCACTCTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGC 89 	90 ACGAGGGACATGCTGGATGATGATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCT 149	150 GCCACAACTCGGCATCCAGAGCCCCGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGG 209	210 CGACCAGTGGCCCTGACCCTGCTGACTTTGTGCTTGGTGCTGATAGGGCTGGCAGCC 269	270 CTGGGGCTTTTGTTTTTT 287 [288 CAGTACTACCAGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAATTA 347

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1 (bases I to 1759)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
CAATGCCTTATAAGCATTCCTTCCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCTCC
                                                                          ATAGGAATTTCTCCCAGGAAAGAAATATATCCCCATCTCCGTTTCATATCAGAACTACCG
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
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/mol_type="mRNA"
/db_xref="reaxon:9606"
/clone="CSODI044YF02"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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llarity 98.3%; Pred. No. 0;
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1 (base 1 to 1045)

2 Li, W.B., Gruber.C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization

L Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30439428.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cramieux, CP 5706 - 91057 ENRY cedex - FRANCE
Email: seqref@genoscope.cns.fr. Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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8X379905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
Clone CSDI041YA14 5-PRIME, mRNA sequence.
BX3779905
TGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATCA 1351
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and RcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                            TTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGTCCAT
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; Score 1027.6; DB 5;
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On May 8, 2003 this sequence version replaced gi:30435570.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
For more information about this cluster, see
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1068 bp mRNA linear EST 23-APR-2004
BX379904 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI041YA14 3-PRIME, mRNA sequence.
BX379904
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1. (Dases 1 to 1068)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

Unpublished (2001)
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitogen.
                                                                                                                               CR604680 1003 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0D1081YG24 of Placenta Cot 25-normalized Of Homo sapiens (human).
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                                                                                                                                                                                                                                                                                                                                                                                                     Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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56.4%; Score 1001.4; DB 3; Length 1003;
Best Local Similarity 99.9%; Pred. No. 8.5e-267;
Matches 1002; Conservative 0; Mismatches 1; Indels 0;
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texon:9606"
/clone="CSODIO81YG24"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Verte
Mammalia, Butheria, Primates, Catarrhini, Hon
1 (Dases 1 to 1003)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Li,W.B., dibraries and normalization
Unpublished
Location/Qualifiers
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CK604680.1 GI:50485487
HTC; CNSLT_CDNA.
HOMO sapiens (human)
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
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sites of the pCMVSPORT 6 vector. Library was normalized.
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http://www.genoscope.cns.fr/cdna?s=CSODI041BA07NP1&c=6541.r.
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99.0%; Pred. No. 5.9e-266;
iive 5; Mismatches 1;
                                                                                     organism="Homo sapiens"
                                                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI041YA14"
                           Location/Qualifiers
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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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14 (basea 1 to 1076)
14, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Ompublished (2001)
On May 8, 2003 this sequence version replaced gi:30435625.
Contact: Genoscope
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a Noti-oligo(dT)
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
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was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster

For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODI067BF07NF1&c=6541.r. Location/Qualifiers

organism="Homo sapiens"

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. [bases 1 to 990]
11,W.B.; Gruber,C.; Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
On May 2, 2003 this sequence version replaced gi:30333765.
Contact: Genoscope

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/mol_type="mrm"_reference //mol_type="mrm" //mol_type="mrm" //mol_type="mrm" //mol_type="mrm" //mol_type="place //molt-type="place //molt-type-//molt-type="place //molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//molt-type-//
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 912.4; DB 5;
Pred. No. 4.9e-242;
5; Mismatches 18;
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BX339074.2 GI:46269380
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Length Indels 861 875 921 815 981 755 1161

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TTTCATGTCTTCCTTACACTTGGTGGAATAAGAAACTTTTTGAAGTAGAGAAATACATT 1281

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RESULT 11 BX339074/c LOCUS DEFINITION

ACCESSION VERSION

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1638 ACCAGAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTATTTTCTTC 1697
/note="1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand CDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pGWVSPORT 6 vector. Library was normalized.
                                                                                                                                    TGAAGCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCC
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                                                                                                                       TTATAATAGATGTCACCAGCCCAAGAAGCAGAGCTGTGTGGCCATCCTTAATGGGATGA
                                                                                                                                                                    Length 996;
                                                                                               Indels
                                                                        Score 912.2; DB 5;
Pred. No. 5.6e-242;
9; Mismatches 19;
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BX358356 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI036YF20 3-PRIME, mRNA sequence.
BX358356
BX358356.2 GI:46287592
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                                                                                                                                                                                                                                                                            ATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCA 1641
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                                                  GAGGTAACATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCC
                                                                                  TICCCAAICCAICAGIAAAGACCCCCAICIGCCIIGICCAIGCCGIIIICCCAACAGGGAIG
                                                                                                                                              TTCCCAATCCATCAGTAAAGACBCCWTCTKCYTTGTCCATGCCKTTTCCCWACAGGGATG
                                                                                                                                                                              154 ATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAGAGAGATTAAAGACCA
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1. 996
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                       GACCCATATTT-ATACCTTTCAGGTACTGAAGAT 1734
                                                                                                                                                                                                                                                                                                                                                                                    sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
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KEYWORDS
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TCGTGTTTCCTGTTCAGGATCACCAGCATTTCTGAGCTTGGGGTTTATGCACGTATTTAAC 1096
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914 bp mRNA linear EST 28-APR-200*
BX391810 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI081YG24 3-PRIME, mRNA sequence.
                                                                              TGAGCTGTATAACAAAGCTGGAGCACACAGGGGCGCGTTGTACAGAACAATGGAAATG 496
                                                                                                       TGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGAAATG 420
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Catarrhini, Hominidae, Homo.
                         TCAAGTCCAGAATATAAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAAACTCTGTCG
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
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Mammalia; Eutheria; Primates;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1049)

1 (bases 1 to 1049)

1 In, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

Unpublished (2001)

On Feb 15, 2001 this sequence version replaced gi:30545374.

Contact: Genoscope - Centre National de Sequencage

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2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Eooky sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="CSODEOGYK19"
/clone="Type="PLACENTA"
/clone_lib="Homo sapins PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a Not1-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was not normalized."
                                                                                                                                         AL541315 Homo sapiens PLACENTA Homo sapiens CST 24-MAR-2004
AL541315 Homo sapiens PLACENTA Homo sapiens CDNA clone CSODE006fYK19
S-FRIME, mRNA sequence.
AL541315
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This sequence belongs to sequence cluster 6541.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODEOO6AF10QP1&c=6541.r.
Location/Qualifiers
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-CATTGACCCATATTTATACCTTTCAGGTACTGA 1730
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18; Mismatches 31;
                         NNNTTGNCCCNGTNTTTTTACTTTCAGGTACTGA
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/db_xref="taxon:9606"
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                              For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSOBA1029ZA09_CS02753_1&c=6541.r
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                                                                                                                                                                                                                                                           /tissue type="Placenta COT 25-NORMALIZED"
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/primer Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
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/clone="CSODI081YG24"
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT & vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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primer. Five prime end enriched, double-strand cDNA was
digested with not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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1 (bases 1 to 1001)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Ompublished (2001)
On May 2, 2003 this sequence version replaced gi:30336406.
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GCCCAAGAAGCAGAGACTGTGTGGGCCATCCTTAATGGGATGATCTTCTCAAAGGACTGCA
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Location/Qualifiers
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l; Mismatches 1;
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/db_xref="taxon:9606"
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180	264	324	384	444	504	564	624	684 660	744	904	864 839	
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Abx75841 1
Abx98044 1
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K, Kojima S, Otsuki
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su A, Sugiyama T, Nagai
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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Wakamatsu A, Sugiyama T,
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AAK94474;
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-MODEL=frame+ p2n.model -DBV=xlp
-MODEL=frame+ p2n.model -DBV=xlp
-G-GSDZ_1/USFTO spool p/US10689742/runat_07102005_183117_27953/app_query.fasta_1.718
-G-CGDZ_1/USFTO spool p/US10689742/runat_07102005_183117_27953/app_query.fasta_1.718
-DB-N Geneseq_16Dec04 -QFWN=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LGOPCL=0
-LIST=E45 -DOCALIGN=200 -THR SCORE-pct - THR MAR=100 -THR MINE-0 - ALIGN=15
-MODE=LCGAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US10689742_@CGN_1 1 886 @runat_07102005_183117_27953 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGG_SCORES=0 -MAXLEN-DSPBALCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADEL -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Ygapop 10.0 , Ygapext
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                                                                                                                                                                  The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5' - and 3' -ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful length clones were obtained by construction of full length cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly
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                                                                                                                              Claim 8; SEQ ID NO 3296; 1380pp + Sequence Listing; English.
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This invention relates to a novel primers useful for synthesising full length cDNA molecules that encode human proteins. Specifically, it refers to secretory or membrane proteins that are potential therapeutic agents/ target molecules in the field of medicine, and in particular genes encoding proteins that are associated with signal transduction, glycoproteins and transcription. The present invention describes a method for efficiently cloning a full length human cDNA from both the 5' and 3' ends using the oligo-capping method. This polynucleotide sequence is a full length human cDNA clone of the invention.
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                                                                                                      CIGITICCATATIATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTT
                                                                                                                                                                          241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg
TTGCCCCCTGACAGTGGCAAGGCCTGTGGATGGAAGGAACCCCTTTCACTTCTGAA
                                                                                                                                                                                                                           784 AATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAAGG
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S, Otsuki T, Koga
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K, Kojima 8
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Wakamatsu A, Sugiyama T, Nagai
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183865.
07-JUL-2000; 2000EP-00114089.
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Treacy M, Agostino MJ, Spaulding
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Best Local Similarity:
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                                                             Homo sapiens
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This sequence encodes a human secreted protein of the invention. The secreted proteins were obtained from human adult placenta, foetal brain, adult testes or adult blood cDNA libraries. The polymucleotides (FNB) and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include mutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating activity, tissue growth activity, activity, haematopoiesis regulating activity, chemotactic/chemokinetic activity, haematopoiesis regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, invasion suppressor activity, and tumour inhibition activity. The PNS are chemokinesis; haemostasis; thrombolysis; anti-inflammatory; gene therapy; tumour invasion suppressor; tumour inhibitor; ss. MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet ä Merberg Sequence 1776 BP; 506 A; 429 C; 370 G; 471 T; 0 U; 0 Other; ú 1776 280 0 0 0 Evans polynucleotides encoding secreted human proteins Length: Matches: Conservative: Mismatches: Racie LA, V; also stated to be useful for gene therapy Indels:

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98US-0088734P
98US-0088734P
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98US-0088741P
98US-0088742P
98US-008874P
98US-008876P
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     TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
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                                                                                                                                                                Membrane-bound protein PRO1131 encoding cDNA.
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The invention provides membrane-bound PRO polypeptides and polynuclectides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK; Yuan J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Membrane-bound proteins and related nucleotide sequences.
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98US-0095311P.
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S S	Sequence	1841 BP;	512 A; 452 C;	387 G; 490 T; 0 L	U; 0 Other;	
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		MetGlnAlaLys	LysTyrSerSerTh	.rArgAspMetLeuAspA	STYTSETSETThrArgAspMetLeuAspAspAspGlyAspThrThrMet	7
	144		zaagtacagcagcac	GAGGGACATGCTGGATC	SATGATGGGGACACCACCATC	20
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È	41	ArgA	SerSerThrTrpAr	gProValAlaLeuThrI	AProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal	1 60
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8			AspThrileSerg1	nMetGluGluArgLeuC	ThrdlydlnAspThr11eSerGlnMetGluGluArgLeuGlyAsmThrSerGlnGluLeu	, ,
q	384		GACACCATTTCTCA	AATGGAAGAAAGATTAG	GAAATACGTCCCAAGAGTTC	-0
ò	101		GlnValGlnAsnIl	eLysLeuAlaGlySer[GlnSerLeuGlnValGlnAsnIleiysLeuAlaGlySerLeuGlnHisValAlaGluLys	B 12(
g	444		caagrccagaarar	AAAGCTTGCAGGAAGTC	recaecarereereaaaa	
& A	121		GluLeuTyrAsnLy 	LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysT 	Y8SerProCysThrGluGln	A 563
8 8	141	H-E	HisGlyAspashCy	BTyrGlnPheTyrLysA	TriveTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp	- '
9 8			CATGGAGACAATTG	CTACCAGTTCTATAAAC	ACAGCAAAAGITGGGAGGAC	- م
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à	201	LeuArgPro	AspSerGlyLysAl	aTrpLeuTrpMetAspG	31 YThrProPheThrSerGlu	1 22(
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ପୁ	864		AAAGGA	ĠĊŔŔŔĠŔŔŢŢĠŔŔĠ	rrerercrerez	923
ò a	261	AlaGlyMetValLysPr gcaggaarggrgaagcc	VallysProGluSe 	rLeuHisValProProG 	roGluSerleuHi8ValProProGluThrleuGlyGluGlyAsp 	280
RESULT AAC9156	[5 561					
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GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
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                                                                                                       1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspAspGlyAspThrThrMet
                                                                                                                                                                                SerLeuHisSerGlnAlaSerAlaThrArgHisProGluProArgArgThrGluHis
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                Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Twenty eight nucleic acids encoding PRO polypeptides which are useful for treating various tumors, e.g. breast cancer, and other inflammatory,
                                                                                                       Human, PRO; cytostatic, nootropic, neuroprotective, respiratory general,
antiinflammatory, antiangiogenic, immunosuppressive, immunostimulant,
PRO agonist, cancer, inflammatory disorder, immunological disorder, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is one of twenty eight nucleic acids encoding PRO polypeptides. The PRO polypeptides and their agonists, including antibodies, peptides, and small molecule agonists, may be used to treat various tumours, e.g., cancers such as breast cancer, ovarian cancer, renal cancer, colorectal cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer, central nervous system cancer, melanoma or leukaemia. They are also useful for treating other disorders such as mecrophagal, epithelial, stronal and blastoccelic disorders, and inflammatory, angiogenic and immunological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Henzel W, Kabakoff RC;
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Matches:
Conservative:
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Wood WI;
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Watanabe CK,
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2000US-0187202P.

2000WO-US006319.

2000WO-US006884.

2000WO-US0088439.
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2000WO-US003565.
2000WO-US004341.
2000WO-US004342.
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99US-0141037P-
99US-014478P-
99WO-US020111
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99WO-US028634-
99WO-US028634-
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99WO-US030095.
99WO-US030999.
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1508.00
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Smith V,
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P-PSDB; AAB50959.
                                                                    Human PRO1131 cDNA
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Percent Similarity:
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18-FEB-2000;
18-FEB-2000;
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02-DEC-1999;
09-DEC-1999;
16-DEC-1999;
20-DEC-1999;
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03-MAR-2000;
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08-SEP-1999;
29-OCT-1999;
30-NOV-1999;
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Pred. No.:
AAC91561;
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prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS21244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to calls expressing PRO polypeptides, to modulate biological activities of calls expressing PRO polypeptides, and to detect the presence of mammalian lung, colon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
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A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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99WO-USO28551.
99WO-USO28564.
99WO-USO28565.
99US-0170262P.
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2000WO-US004341.
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2000WO-US004414.
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2000US-0209832P
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Stewart TA,
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06-JAN-2000;
06-JAN-2000;
11-FEB-2000;
18-FEB-2000;
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03-MAR-2000;
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15-MAR-2000;
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09-DEC-1999;
16-DEC-1999;
20-DEC-1999;
30-DEC-1999;
30-DEC-1999;
                                                Homo sapiens
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22-FEB-2000;
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Smith V, St
                                                                                            07-JUN-2001
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breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a call sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from cartilage, the proliferation of inner ear utricular supporting cells or of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor (VIA). The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymorlectides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA,
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                                                                                                                                                                                                                                                                  transgenic or knock out animals and can be used in gene therapy
                                                                                                                                                                                                                                                                                                         Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;
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Matches:
Conservative:
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CTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAA 563
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CTGTTCCATATTATATAGTCACCAGCCCAAGAGCAGAGAGACTGTGTGGCCATCCTC 863
                                                                               GCAGGAATGGTGAAGCCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCGAAGGTGAC 983
                                                                                                                                                                                                       PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss; dog; cat; pig; goat; rabblt; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prosteate; rectum; cervix; liver; genetic disorder;
                                         AATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTTTTTTGTAGAAGAAGAA
                              AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg
                                                                   AlaGlyMetVallysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp
                                                                                                                                                                                      Human DNA encoding PRO polypeptide sequence #301.
                                                                                                                            AAS46225 standard; cDNA; 1841 BP
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2000US-0193032P.
2000US-0193053P.
2000WO-US008439.
2000US-0194449P.
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2000US-0199397P.
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                                                                                                                                                                 (first entry)
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03-MAR-2000;
06-MAR-2000;
14-MAR-2000;
14-MAR-2000;
15-MAR-2000;
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21-MAR-2000;
21-MAR-2000;
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11-APR-2000;
11-APR-2000;
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08-NOV-2000;
01-DEC-2000;
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18-APR-2000;
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25-APR-2000;
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primers for PRO polypeptides of the invention. The sequences of the primers for PRO polypeptides of the invention. The sequences of the invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, hung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
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                                                                                                                                                                                                                                                                                                  Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and screen for modulators of the compounds.
                                                                                                                         Gurney AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 AGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGCGCGCACAGAGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MetGlnalaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis
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                                                                                                                      Godowski PJ,
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Watanabe CK, Wood WI, Zhang Z;
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Matches:
Conservative:
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20-DEC-2000; 2000WO-US034956
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                                                            (GETH ) GENENTECH INC
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Query Match:
DB:
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                                                                                                                                                                         AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
                623
                               CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180
                                         684 CTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTT 743
                                                                                                       LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240
                                                                                                                                                                                            AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
                                                                                                                                                                                                     GCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCGAAGGTGAC 983
                                                                                                                                                                                                                                                                                                         Human; secreted and transmembrane protein; PRO; cytostatic; cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
                                                                                             LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu
         LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu
                                                                                                                                                                                                                                                                                          Human PRO1131 (UNQ569) nucleotide sequence SEQ ID NO:318.
                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US012252.
99US-0141037P.
99US-0144758P.
99US-014568P.
99US-014668P.
99US-0146522P.
99WO-US021590.
99WO-US021547.
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24-FEB-2000; 2000WO-US004914.
24-FEB-2000; 2000WO-US005004.
02-MAR-2000; 2000WO-US006884.
15-MAR-2000; 2000WO-US006884.
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99WO-US028301,
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2000WO-US003565.
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                                                                                                                                                                                                                                                                                                                          diagnostic assay; ss
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11-FEB-2000;
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15-SEP-1999;
08-OCT-1999;
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proteins. The PRO proteins have cycostatic activity. The PRO proteins can radiolabels or antibodies, that cause cell death. PRO proteins, radiolabels or antibodies, that cause cell death. PRO nucleotide chromosomal and gene mapping, and in the generation of anti-sense RNA and chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the issolation of human PRO sequences. AAF44675 to AAB65300 represent human PRO belynucleotide and protein sequences given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
                                                                                                                                                                     1 DL;
Godowski PJ;
Paoni NF;
M, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention describes human secreted and transmembrane
                                                                                                                                                                         Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton I
Ferrara N, Fong S, Gerber H, Gerriteen ME, Goddard A, Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Roy MA, Stewart TA, Tunas D, Watanabe CK, Williams PM,
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20-MAR-2000; 2000WO-US007377.
                                                                                         (GETH ) GENENTECH INC.
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Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other; 1841 280 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: 3.3e-147 1508.00 100.00% 100.00%

(1-1841)US-10-689-742-160 (1-280) x AAF44218

Gaps:

		MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspAspGlyAspThrThrMet 20	
	144		
	23	SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40	
	20,	204 AGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGCGCCACAGAGCAC 263	
	4	ArgalaproSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60	
ž	7 564	264 AGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTTGTGCTTTGTG 323	
	9	61 LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsn 80	
	324	CTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTTTTTTTT	
	81		
	384		
	. 103	GINSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120	
	44	444 CAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA 503	
	12:	121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140	

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(GETH ) GENENTECH INC.
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                      20-DEC-2000; 22-JAN-2001; 28-FEB-2001; 28-FEB-2001; 01-MAR-2001; 09-MAR-2001; 214-MAR-2001; 2
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05-APR-2001;
10-MAY-2001;
10-MAY-2001;
25-MAY-2001;
25-MAY-2001;
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                                                         TGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAC
                                                                                                                                                                     TGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAAAAAAGAAGAC
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                         TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp
                                                                                                                                   CyslysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp
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01-DEC-2000;
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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85031. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hyportension, arterial restenosis, rhemmatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tummour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABU88259 to ABL88267 represent primers and probes used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goddard A;
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2000WO-US034956.
2001US-00767609.
2001US-0076498.
2001WO-US006520.
2001WO-US006666.
2001US-00808689.
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2001US-00828366.
2001US-00854208.
2001US-00854280.
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atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
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antiarteriosclerotic; gene; sse
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                                                        ACTGGTCAAGACACCATTTCTCAAATGGAAGAAGATTAGGAAATACGTCCCAAGAGTTG
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02-AUG-2000;
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PR 15-187-2000; 20008-20209789-
PR 18-287-2000; 20008-2020978-
PR 18-287-2000; 20008-2020978-
PR 18-287-2000; 20008-202092-
PR 20-287-2000; 20008-202092-
PR 20-287-200092-
PR 20-287-200092-
PR 20-287-20092-
PR 20-287-20092-
PR 20-287-20092-
PR 20
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Length:

3.3e-147

breast;

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Human; PRO polypeptide; secreted protein; transmembrane protein; chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical; liver; cancer; TRF-alpha; tumour necrosis factor-alpha; proliferation; differentiation; chondrocyte cell; bone disorder; cartilage disorder; sports injury; arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
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18-SEP-1997;
21-0CT-1997;
24-0CT-1997;
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28-0CT-1997;
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24-NOV-1997;
11-DEC-1997;
12-DEC-1997;
14-DEC-1997;
18-DEC-1997;
10-MAR-1998;
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                                                                              MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspAspGlyAspThrThrMet
                                                                                                                                                                                                  LeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsn
                                                                                                                                                                                                             ACTGGTCAAGACACCATTTCTCAAATGGAAGAATTAGGAAATACGTCCCAAGAGTTG
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                                                                                                  ATGCAGGCCAAGTACAGCAGCACGAGGACATGCTGGATGATGATGGGGACACCATG
                                                                                                                                                           ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal
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98US - 0086486P 98US - 0087098P 98US - 0087208P 98US - 008759P 98US - 0088025P 98US - 0088025P 98US - 0088023P 98US - 0088023P 98US - 0088023P 98US - 0088023P 98US - 0088021P 98US - 0088212P 98US - 0088212P 98US - 0088718P 98US - 0088811P 98US - 0088814P 98US - 0088814P	0088861P. -0088876P. -008876P. -0089105P. -0089514P. -0089538P. -0089538P. -0089538P. -0089528P. -0099524P. -0090524P. -0090444P. -0090541P. -0090548P. -0090678P.		0091486P. 0091626P. 00916328P. 0094006P. 0095282P. 0096757P. 0096766P. 0096766P. 0096891P. 0096891P.

22-MAY - 1998 | 28-MAY - 1998 | 28-MY - 1998

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                     ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu
                                                   CAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCAGCATGTGGAAAAA
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98WO-US01930.
98WO-US021141.
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16-SEP-1998;
07-OCT-1998;
07-OCY-1998;
01-DEC-1998;
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The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane), sequences 80% identical to them, or encoding a PRO polypeptide lacking its associated signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Three hundred and five nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, and for detecting
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and WI, Zhang Z;
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or an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide. Also included are the encoded PRO proteins, CC PRO expression vectors, host calls transformed with the vector (used to produce PRO proteins), a chimaeric molecule comprising the PRO proteins), a chimaeric molecule comprising the PRO produce PRO proteins), a chimaeric molecule comprising the PRO proteins), a chimaeric molecule comprising the PRO proteins), a chimaeric molecule comprising the PRO proteins), a chimaeric molecule control network of the PRO alpha (TMP-alpha) from human blood (by contacting the blood with PRO1079, PRO427, PRO4181, PRO1181, PRO 1182, PRO1182, PRO1
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Sequence 1841 BP; 512 A; 452 C; 387 G; 490 T; 0 U; 0 Other;

1841	280	0	0	0	0
Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 8 Gaps: 0	742-160 (1-280) x ACA73685 (1-1841)	1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet 20	144 ATGCAGGCCAAGTACAGCACGCACGACATGCTGCATGATGATGAGGGACACCATG 203	21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40	204 AGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGCGCACAAGAGCAC 263	41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 60	264 AGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGCTGACTTTGTGCTTGGGT 323	61 LeuLeulleGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsn 80	324 CTGCTGATAGGGCTGGCGGGGCCTTTTTTTTTTTTTTTT	81 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100	384 ACTGGTCAAGACACCATTTCTCAAATGGAAGGAAGGAATGGAATTAGGAAATACGTCCCAAGAGTTG 443	101 GinSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120	444 CAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA 503	121 LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln 140	504 CTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCTGTCTTGTACAAAGCAA 563	141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160	
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564 IGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGAC 623	61 CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 	181 LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu 200 	201 LeuhrgProAspSerGlyLysalaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220	221 LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 240 	241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260	261 AladiyMetValLyaProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280	SULT 13 \\06000ACA06000 standard; cDNA; 1841 BP.	ACA06000;	Y-2003 (first entry)	secreted/transmembrane protein (PRO) cDNA #301.	Human; gene; 88; secreted and transmembrane protein; PRO; TNF-alpha; tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing.	Homo sapiens.	US2003036162-A1.	0-FBB-2003.	2002US-001944	-JUN-1998; -SEP-1998;	-OCT-1998;	-NOV-1998;	-DEC-1998;	-MAR-1999;	-MAY-1999;	-AUG-1999;	-AUG-1999; -AUG-1999;	25-AUG-1999; 99US-00380142. 01-SEP-1999; 99WO-US020111.	-SEP-1999; -OCT-1999;	-NOV-1999; -DEC-1999;	-DEC-1999;	-JAN-2000: 2000WO-US0312/		-FEB-2000: 2000WO-US00434
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transmembrane (PRO) polypeptides. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TWF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TWF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the presence of a cumour in a mammal and an oligonucleotide probe derived from any of the PRO mucleotide sequences. The nucleotide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for etimulating the release of TNF-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes and cetting the proliferation or differentiation of chondrocytes and cetting the presence of a tumour. The PRO polypeptides and nucleic acids may also be used diagnostically for tissue typing. The sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      " secreted and transmembrane PRO polypeptides and nucleic acids, useful gene therapy, in chromosome and gene mapping, as chromosome markers, tissue typing, and in chromosome identification.
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stanabe CK, Wood WI, Zhang Z;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp
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presented in ACA05700-ACA06004 are the cDNAs encoding the PRO polypeptides of the invention
                                               Other;
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GlnSerLeuGlnValGlnAenIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys 120
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                                                                                                                                                                                                                                                                                                                                    transmembrane
                                                                                                                                                                                                                                                                                                                                 Three hundred and five nucleic acids encoding secreted and transmembrane PRO polypeptides, useful for the diagnosis, prevention and/or treatment of tumors, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumors.
                                                                                                                                                                                                                                        Gurney AL;
                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to three hundred and five nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 AGCCTGCATTCTCAAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGGGGCACAGAAGCAC
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                                                                                                                                                                                                                                       Godowski PJ,
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, Wood WI, Zhang
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                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 601; 708pp; English.
             29-JUN-2001; 2001WO-US021066.
09-JUL-2001; 2001WO-US021735.
18-JUL-2001; 2001US-00918827.
30-JUL-2001; 2001US-009188827.
13-AUG-2001; 2001US-00924419.
13-AUG-2001; 2001US-00929404.
16-AUG-2001; 2001US-00941992.
28-AUG-2001; 2001WS-00941992.
29-AUG-2001; 2001WS-00941992.
04-SEP-2001; 2001WS-00941992.
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Smith V, Watanabe CK,
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Pan J, S
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                                                                                                                                           colon; breast; prostate; rectal; cervical;
                                                                                                          cDNA encoding human PRO protein #301
                                                                                                                                                           PRO; gene therapy; gene; ss
                ACA66834 standard; cDNA; 1841 BP
                                                                                                                                           tumour; adrenal; lung;
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98WS-00187368.
98WO-USO25108.
98US-00202054.
99US-00254311.
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99US-00311832.
99WO-US010733.
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99US-00380142.
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2000US-00664610
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18-FEB-2000;
22-FEB-2000;
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01-MAR-2000;
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14-MAY-1999;
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99WO-US028313.
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99WO-US028634.
99WO-US030095.
99WO-US030911.
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2000WO-US004914.
2000WO-US005004.
  98US-0087827P
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2000WO-US032678
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15-MAR-2000;
20-MAR-2000;
30-MAR-2000;
15-MAY-2000;
17-MAY-2000;
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11-FEB-2000;
22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
02-MAR-2000;
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08-NOV-2000;
01-DEC-2000;
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11-JUN-1998;
11-JUN-1998;
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12-JUN-1998;
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 CAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted and transmembrane protein; cytostatic; anti-HIV; virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy; prof. pharmaceutical; diagnostic; biosenoor; bioracator; malignancy; cancer; outsian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia; lymphoma; hepatitis B; multiple sclerosis; Crohn's disease; drug screening; gene; ss.
                     LeuCygArgGluLeuTyrAgnLygAlaGlyAlaHisArgCygSerProCygThrGluGln
                                                                                                                                                                                                                                               CIGITICCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTC
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                                                                        CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp
                                                                                                                  CTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGCTT
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97US-0062250P.
97US-0065186P.
97US-0065311P.
97US-0065311P.
98US-0078910P.
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98US-008106P.
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05-NOV-1997,
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02-JUN-1998,
02-JUN-1998,
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The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American CTPC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA, 209439, 203135, etc); or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are useful as pharmaceutricals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma, leusease in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human colMa, genemic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This sequence encodes a novel human secreted
                                                                                                                                                                                                                                                                                                                                                                                                        New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's
                                                                                                                                                                                                       DL;
Godowski PJ;
                                                                                                                                                                                                                                                 Paoni NF;
Wood WI;
                                                                                                                                                                                                     Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton I
Berzara N, Rong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, I
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 229; 663pp; English.
28-FEB-2001; 2001MO-US006520.
01-UTN-2001; 2001MO-US017800.
20-UTN-2001; 2001MO-US019692.
9-UTN-2001; 2001MO-US021066.
09-UTL-2001; 2001MO-US021735.
28-AUG-2001; 2001US-00941992.
                                                                                                                                                         (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                       WPI; 2003-352829/33.
P-PSDB; ABU72542.
                                                                                                                                                                                                                                                                                             Zhang Z;
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512 A; 452 C; 387 G; 490 T; 0 U; 0 Other; Sequence 1841 BP;

and transmembrane PRO polypeptide

144 ATGCAGGCCAAGTACAGCAGCACGAGGACATGCTGGATGATGATGAGGGACACCACCATG 203 204 AGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAAGCCCCGGGGCACAGAGCAC 263 264 AGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGCTGACTTTGTGCTTGGTG 323 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis LeuteulleGlyteuAlaAlaLeuGlyteuteuPhePheGlnTyrTyrGlnLeuSerAsn 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal 1841 280 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: US-10-689-742-160 (1-280) x ACA64371 (1-1841) 3.3e-147 1508.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: 21 41 61 81 Query Match: DB: ઠ 셤 8 d ઠે g ð g

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Carlotte State

200 220 240 260 924 GCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCGAAGGTGAC 444 CAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 624 IGHIANTITICIGCCTTAGTGAAAAACTCTACCATGCTGAAGAAGAAAAACAAAGAAGAAGAA LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu 241 AsnGlyMetIlePheSerLyBAspCysLysGluLeuLyBArgCysValCysGluArgArg AlaGlyMetValLysProGlySerLeuHiBValProProGluThrLeuGlyGluGlyAsp 384 ACTGGTCAAGACACCATTTCTCAAATGGAAGAAGATTAGGAAATACGTCCCAAGAGTTG 564 TGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGAC CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 864 AATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAAGG GlnSerLeuGlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLys cregaarricececercreaaceracreraarrirrreracrerrarreaacaedecrr 161 181 221 684 201 744 261 ò g g g 셤 g 셤 ઠે ઠે ò ઠે 셤 ò 셤 ò ð ઠ

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AX376534 Sequence
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BC057746 Homo sapi
BD194489 Humanized
AX77295 Sequence
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CO781749 Sequence
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BD12512 Primer fo
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AX076248 Sequence
AX104772 Homo sapi
BD059332 Secreted
AX376526 Sequence
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AX168243 Homo sapi
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AX168243 Homo sapi
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BC064054 Mus muscu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primers for synthesizing full length cDNA clones and their use Patent: EP 1396543-A 3296 10-MAR-2004; Research Association for Biotechnology (JP) Location/Qualifiers
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Seguence 3296 from Patent EP1396543.
CQ783156
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VERSION
KEYWORDS
SOURCE
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AUTHORS
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-MODEL=frame+ pl.n.model -DEV=xlp
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AK075114 Homo sapi
BD074859 Secreted
                                                                                                ' Search time 4253.3 Seconds
(without alignments)
3189.870 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                      OM protein - nucleic search, using frame plus p2n model
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Maximum DB seq length: 200000000
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Database :

Score

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Total number of

Searched:

Perfect score:

Title:

Run on:

Sequence:

Scoring table:

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GEGD"
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                                                                                                                                                                                                                                                                                                                                               07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
(base 1 to 1756)
Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y.,
Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
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                                                                                                                                                                                                                                             Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 2934 22-JAN-2002; HELIX RESEARCH INSTITUTE
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full-length cDNA and use
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Location/Qualifiers
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JP 2002017375-A/2934
22-JAN-2002
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                                                                                BD127503.1 GI:23222448
JP 2002017375-A/2934.
Homo sapiens (human)
Homo sapiens
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PN JP 200201737
PD 22-JAN-2002
PF 07-JUL-2000
PI TOSHIO OTA,T.
PI STHI,
PI YURI KAWAI,A
SHINICHI KOJIMA,
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                                   /tissue_type="placenta"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AK075114 1756 bp mRNA linear PRI 03-SEP-2002 Homo sapiens cDNA FLJ90633 fis, clone PLACE1003573, weakly similar to T-CELL SURFACE GLYCOPROTEIN YE1/48.
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Catarrhini, Hominidae, Homo.
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                                                                                                                     TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp
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CTCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGGGGGCGCCCTTGTACAGAACAA
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Homo sapiens

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Isogai, T. and Otsuki, T.
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S Bollinger, C.L. Jr.

Crane test weight assembly and method

AL Patent: US 6725730-A 457 27-APR-2004;

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Sequence 457 from patent US 6725730.
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Conservative:
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 /mol_type="genomic I" US-10-689-742-160 (1-280) x AR528680 7.22e-147 1508.00 100.00\$ 100.00\$

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                                                                                                            CyslysTyrPheCysLeuSerGluAsnSerThrMetLeulys1leAsnLysGlnGluAsp 180
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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CAATCTTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA
                                                                                564 TGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGAC
                     LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln
                                                                                                                                  LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 318 from Patent WO0073454.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                              41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal
                                                                                                                                                                  LeuleulleGlyleuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsn
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SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis
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PAT 16-JUL-2002

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Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E., Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K., Wood, W.L. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
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Patent: WO 0208284-A 165 31-JAN-2002; decentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerriteen, Mary E. (US); Goddard, Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US); Fandrh J. (US); Scophan, Jean-Philippe F. (US); Faoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US); Matanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
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Qy 141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160 Db 564 TGGAAATGGCATGGAGACAACTGCTACTATAAGACACAGCAAAAGTTGGGAGGAC 623 Qy 161 CysLySTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp 180 Db 624 TGTAAATATTCTGCCTTAGTGAAAACTCTACCATGCTGAAGAAAAAAAA	201 LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu 220 11	OY 221 LeubnislielleleisbyalThisErProArgschaftscheu 240 DD 804 CTGTTCCATATTATAATAGATGACCAGCCCAAGAAGACGAGAGCTGTGGGCCATCCTC 863 OY 241 AsnGlyMetilePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260	Oy 261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280	RESULT 12 AX491058 LOCUS AX491058 AX491058 ACTINITION Sequence 165 from Patent W00200690. ACTESSION AX491058 VERSION AX491058.1 G1:22323866 KEYWORDS CONDERS CONDES CONDERS CONDERS CONDES CONDERS CONDERS CONDERS CONDERS CONDERS CONDERS CON	_	AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.	TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis JOURNAL Patent: WO 0200690-A 165 03-JAN-2002; Genentech, Inc. (US)	FEATURES Location/Qualifiers 1. 1841 / Organism="Homo sapiens" / mol_type="Hussigned DNA" / db_xref="taxon:9606"	Alignment Scores: 7.22e-147 Length: 1841 Pred. No.: 7.22e-147 Length: 1841 Score: 1508.00 Matches: 280 Percent Similarity: 100.00\$ Conservative: 0 Best Local Similarity: 100.00\$ Mismatches: 0 Query Match: 6 Gaps: 0	US-10-689-742-160 (1-280) x AX491058 (1-1841) Qy	Qy 21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis 40

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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haich, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Ran, S.J., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Hordy, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Willalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Kzzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.B.
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GCAGGAATGGTGAAGCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCGAAGGTGAC 983
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Submitted (19-MBA-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                         684 CIGGAATTIGCCGCGTCTCAGAGCTACTCTGAGITTITTCTACTCTTATIGGACAGGGCTT
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Tissue Procurement: Dr. Stefan Hansson
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                  2 (bases 1 to 1841)
Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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MARMADORA; NECEAZOA; LIDIZUARIA; VETEDIZACIA; DELEGRACIA; DELEGRACIA; DELEGRACIA; LIDIZUARIA; VETEDIZACIA; DELEGRACIA; DELEGRACIA; DELEGRACIA; DELEGRACIA; DELEGRACIA; DELEGRACIA; STRAUBERGY, E.D., Felingold, E.A., Grouse, L.H., Derge, J.G., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Diatchenko, L., Marusina, K., Farmer, A.A., Subhin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheitz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., McEwan, P.J., McKernan, K.J., Malek, J.A., Gusaranne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Barchard, G., Blakesley, R.W., Touchman, J.W., Green, E.D., Butterfield, Y.S., Krzywinski, M., Touchman, J.W., Green, E.D., Butterfield, S., Krzywinski, M.I., Skalaka, U., Smailus, D.E., Schmerch, A., Schein, J.E., Jones, S.J. and Marza, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HC039072 1797 bp mRNA linear PRI 30-JUN-2004
Homo sapiens C-type lectin-like receptor-1, mRNA (cDNA clone
MGC:34328 IMAGE:5178017), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         664 TTGCGCCCTGACAGTGGCAAGGCCTGGCTGTGGATGGAACCCCCTTTCACTTCTGAA 723
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Submitted (01-NOV-2002) National Institutes of Health, Mammalian
                                              141 TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp
                                                                                                                                                                      484 TGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGAC
                                                                                                                                                                                                                                                                                                                    LeudrgProAspSerGlyLyBAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 AsnGlyMetIlePheSerLyBAspCysLyBGluLeuLyBArgCysValCyBGluArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   784 AATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       844 GCAGGAATGATGAAGCCAGAGAGCCTCCATGTCCCCCCTGAAACATTAGGCGAAGGTGAC
      364 CAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA
                                                                                                                                                                                                                              CyslysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp
                                                                                                                                                                                                                                                            LeuPheHis1le1le1leAspValThrSerProArgSerArgAspCysValAla1leLeu
                                                                                                                                                                                                                                                                                                                                                                604 CTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences
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TITLE
JOURNAL
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AUTHORS
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                                                                                                        Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LIANL at: http://image.llnl.gov Series: IRAK Plate: 168 Row: k Column: 9 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 23503120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STWRPVALTILITICIVILIGIAALGILFPQYYQLSNTGQDTISQMEERIGNTSQELQS
LQVQNIKLAGSLQHVAEKLCRELYNKAGAHRCSPCTEQWKWIGDNCYQFYKDSKSWED
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SELFHIIIDVTSPRSRDCVAILNGMIFSKDCKELKRCVCERRAGMVKPESLHVPPETL
GEGD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MQAKYSSTRDMLDDDGDTTMSLHSQASATTRHPEPRRTEHRAPS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrGlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeu 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 AGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGGGCACAGAGCAC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 ACTGGTCAAGACACCATTTCTCAAATGGAAGAATAAGAAATACGTCCCAAGAGTTG 363
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Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal
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Indels:
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/gene="CLEC1"
/note="gynonym: MGC34328"
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64. .906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="CLEC1"
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CKYFCLSENSTWLKINKQEDLEFAASQSYSBFPSYSYWTGLLARDSGRXWLWMDGTPFT
SELFHIIIDVTSPRSRDCVALINGMIFSKDCKELKRCVCERRAGMVKPBSLHVPPFTLGEGD
                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 51 Row: o Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7706062.
Location/Qualifiers
                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center.
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATGGAGGGACACCATG 109
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                Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis
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Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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                                                  URL: http://mgc.nci.nih.gov
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Conservative:
Mismatches:
Indels:
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                                                    NIH-MGC Project URL: ht
Contact: MGC help desk
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931, App 1, Appli 1, Appli 27, Appl

4430, Ap

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Sequence 4090, Ap
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Sequence 14, Appl
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APPLICANT: Patterson, Chandra
APPLICANT: Patterson, Chandra
APPLICANT: Corley, Neil C.
APPLICANT: Sather, Susan
TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESSE: Incyte Pharmaccuticals, Inc.
STREET: 3174 Porter Dr.
US-08-772-440-1
US-08-966-316-15
US-08-168-316-15
US-09-113-748-2
US-09-113-748-2
US-09-1013-748-19
US-09-988-554-19
US-09-898-554-12
US-09-898-554-11
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FastSEQ for Windows Version 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/055,095
FILING DATE: Filed Herewith
PRIOSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/09055095; Patent No. 5945308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BIllings, Lucy J.
REGISTRATION NUMBER: 36,749
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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Sequence 52,
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Sequence 3
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/cgn2_6/ptcdata/1/ina/5B_COMB.seq:*
/cgn2_6/ptcdata/1/ina/6A_COMB.seq:*
/cgn2_6/ptcdata/1/ina/6B_COMB.seq:*
/cgn2_6/ptcdata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptcdata/1/ina/PcTUS_COMB.seq:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                     OM protein - nucleic search, using frame_plus_p2n model
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US-09-247-155-52
US-08-690-095-2
US-09-113-789-2
US-09-016-434-800
US-09-482-273-34
US-08-809-494A-1
US-08-809-494A-3
US-08-809-494A-3
US-08-809-494A-5
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Listing first 45 summaries
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Database :

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Sequence:

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ORGANISM: Homo sapiens
FEATURE:
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; LOCATION: 806..821
US-09-247-155-52
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Matches:
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                                                                                                                                                     Gaps:
TELEFAX: 650-845-4166
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 1740 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGNOT09
CLONE: 1355922
                                                                                                          1.4e-171
1465.00
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                         RESULT 2
US-09-247-155-52
Sequence 52. Application US/09247155A
Patent No. 6312922
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
TITLE OF INVENTION: Complementary DNAS
FILE REFERENCE: GENSET. 021A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT APPLICATION NUMBER: 06/074,121
EARLIER APPLICATION NUMBER: 60/074,121
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: Patent.pm
SEQ ID NO 52
EENTH: PATENTH: PATENTH
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                                                                                                                                        HisValProProGluThrLeuGlyGluGlyAsp 280
                                                                                                                                                                                   845 CAIGTCCCCCCTGAAACATTAGGCGAAGGIGAC
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Matches:
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FEATURE:
FOCATION: 46..732
LOCATION: 46..732
RABATURE:
FOCATION: 46..186
COTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: Seq LILLILCVGMVVG/LV
FEATURE:
FOCATION: 781..786
LOCATION: 781..786
FEATURE:
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| ATAAATAGACTATATGTTCAATATTATCACTGCACTTATAAAAAAGAATGATGATGTGAG
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Matches:
Conservative:
Mismatches:
Indels:
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    S
    PF-0110
REFERENCE/DOCKET NUMBER: PF-(
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: 81ngle
                                                                                                                                                                                                                                                  355.50
49.80%
35.22%
23.57%
                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: MPHGNOTO3
CLONE: 513418
                                                                                                                                                                                                                                                                               Best Local Similarity:
                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                              US-08-690-095-2
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                                           207
                                                                86 IleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGlnSerLeuGlnVal 105
                                                                                                                                                                            ------GlubeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGlu 139
                                                                                                                                                                                                                                                   478 ATTGTGGAGTACATCAAAGCCAGGACTCAT-----TTAATTCGTTGGGTCGGA 525
                                                                                                                                                                                                                                                                                                                                                                                                      LeuLeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSer 219
                                                                                                                                                                                                                                                                                                                                                                                                                         GlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLysLeuCysArg---- 123
                                                                                                                                                                                                                                                                                         160 AspCysLyrPheCysLeuSerGluAenSerThrMetLeuLyslleAsnLysGlnGlu 179
                                                                                                                                                                                                                                                                                                        ::: ||| :::||| :::||| 418 GAGAGTACTGCCACTGACATGCTACTCTCCTGAAGATTGACAACCGGAAC 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 LeuAsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArg 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    640 CATAATGGGAAAATGCACCCTACCTTCTGTGAGAACAAAAATTTTAATGTGTGAGAGG 699
                                                                                                                                                                                                         298 GTAAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCTGTGTGACACA 357
                              GTGGCTCTGGGGATTTTGG
                                                                                             ---rcrgrcargcagcgcaartac-------------------------------
                                                                                                                                          AlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThrGlyGlnAspThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08690095
Patent No. 5792648
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111 AlaGlySerLeuGinHisValAlaGluLysLeuCysArgGluLeuTyrAsnLysAlaGly 130 102 -----SerLeuGlnVal-----GlnAsnIle-------LysLeu 110 519 GAGCACAAATGTAAGCCTTGTCCAAGGAGATGGATTTGGCATAAGGACAGCTGTTATTTC 578 240 écrecercicargrandecerceageaecerrerrereacercerrerere 299 131 AlaHisArgCysSerProCysThrGluGlnTrpLysTrpHisGlyAspAsnCysTyrGln 150 PheTyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSer 170 171 ThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaAlaSerGlnSerTyrSer 190 699 -----TATGACTATTGGCTGGGATTATCTCCTGAAGAAGATTCCACTCGTGGTATG 749 202 ArgProAsp-----SerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThr 218 SerGluLeuPheHisIleIleleAspValThrSerProArgSerArgAspCysValAla 238 807 AATAACATGTAT----TGTGGATAT 827 239 IleLeuAsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGlu 258 62 LeuileGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThr 82 GlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGln 42 AlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeu

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--GlnAsnile
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 -----SerLeuGlnVal----
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                               807 AATAACATGTAT----
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 GCTCCCTCTCATGTATGGCGTCCAGCAGCCTTGTTTCTGACTCTTCTGTGCCTTCTGTTG 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCATTGGATTGGGAGTCTTGGCAAGCATGTTTCATGTAACTTTGAAGATAGAA----- 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyGlnAspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGln 101
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87
36
77
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                                                                                                             GENERAL INFORMATION:
APPLICANT: Hilman, Jennifer L.
APPLICANT: Hilman, Jennifer L.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
Indels:
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Matches:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,789
FILING DATE:
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APPLICATION NUMBER: 08/690,095
FTILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-655
 259 ArgArgAlaGlyMetValLys 265
                           888 AAGATGCCCAATCCAGTGCAG 908
                                                                      US-09-113-789-2
; Sequence 2, Application US/09113789
; Patent No. 6034219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2:
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355.50
49.80%
35.22%
23.57%
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415-845-4166
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LIBRARY: MPHGNOT03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CON OPERATING SYSTEM:
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Best Local Similarity:
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Pred. No.:
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--LysLeu 110
                                                                                                           111 AlaGlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTyrAsnLysAlaGly 130
                                                                                                                                                                                                                                131 AlaHisArgCysSerProCysThrGluGlnTrpLysTrpHisGlyAspAsnCysTyrGln 150
                                                                                                                                                                                                                                                                                       519 GAGCACAAATGTAAGCCTTGTCCAAGGAGATGGATTTGGCATAAGGACAGCTGTTATTTC 578
                                                                                                                                                                                                                                                                                                                                                                                    579 CTAAGTGATGATGTCCAAACATGGCAGGAGTAAAATGGCCTGTGCTGCTGAGAATGCC 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            202 ArgProAsp-----SerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThr 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  750 AGAGTGGATAATATAATCAACTCCTGCCTGGGTT---ATAAGAAACGCACCTGACTTA 806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 SerGluLeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAla 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191 GluPhePheTyrSerTyrTrpThrGlyLeu---------------------------Leu 201
                                    171 ThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaAlaSerGlnSerTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 IleLeuAsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151 PheTyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSer
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Sequence 800, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CONTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459 TCCACCACACTGCAAACAATAGCCACCAAATTATGTCGTGAGGCTATATAGCAAAGAACAA 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 AlaHisArgCysSerProCysThrGluGlnTrpLysTrpHisGlyAspAsnCysTyrGln 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              519 GAGCACAAATGTAAGCCTTGTCCAAGGAGATGGATTTGGCATAAGGACAGCTGTTATTTC 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579 CTAAGTGATGATGACCAAGAACAGGAGAGAGAAAAATGGCCTGTGCTGCTGCTGAGAATGGC 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 ThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaAlaSerGlnSerTyrSer 190
                                                                                                                                                                                                                                                                                                                                                                                          240 gerecerereargrangogreceageageerrerreragaerererergeeerrerrer 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 PheTyrLysAgpSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSer 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           219 SerGluLeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAla 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 IleLeuAsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGlu 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------TĠTGGATAT 827
                                                                                                                                                                                                                                                                                                                                                                                                                      62 LeuileGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThr 81
                                                                                                                                                                                                                                                                                                                                                                 42 AlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeu 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             750 AGAGTGGATAATATAATCAACTCCTCTGCCTGGGTT----ATAAGAAACGCACCTGACTTA
                                                                                                                                                                                                                                        970
87
36
77
47
                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                       US-10-689-742-160 (1-280) x US-09-016-434-800 (1-970)
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 800:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              807 AATAACATGTAT-----
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355.50
49.80%
35.22%
23.57%
                                                                                                                                                                     LIBRARY: MPHGNOT03
CLONE: 513418
                                                                                                                                                                                                                                                                        Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
                                                                                                                                                                                                US-09-016-434-800
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406 ------ATGAAAAATGAACAACTACAAAACTCAGTGAAGAGCTCCAG 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 AlaGlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTyrAsnLysAlaGly 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 AlaHisArgCysSerProCysThrGluGlnTrpLysTrpHisGlyAspAsnCysTyrGln 150
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                              GEMERAL INCURRALLOUS.

JAPLICANT: Rosen et al.

TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P2030P1
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER APPLICATION NUMBER: 60/092,922
EARLIER APPLICATION NUMBER: 60/092,926
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 60/092,936
EARLIER APPLICATION NUMBER: 00/092,936
EARLIER PILING DATE: 1998-07-15
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10_689-742-160 (1-280) x US-09-482-273-34 (1-1737)
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                                         888 AAGATGCCCAATCCAGTGCAG 908
                                                                                                                                  Sequence 34, Application US/09482273
Patent No. 6534631
GENERAL INFORMATION:
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259 ArgArgAlaGlyMetValLys
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351.50
49.80%
34.82%
23.31%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1731)
; OTHER INFORMATION:
US-09-482-273-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: SITE
LOCATION: (1674)
OTHER INFORMATION:
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FEATURE:
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                                                                                     SerGluLeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAla 238
                                                                                                                                                                                                                                                                                                                                    239 ileLeuAsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGlu 258
151 PheTyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSer 170
                                                                171 ThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaAlaSerGlnSerTyrSer 190
                                                                                                                                  -----TATGACTATTGGCTGGGATTATCTCCTGAAGAAGATTCCACTCGTGGTATG 801
                                                                                                                                                                                                    ArgProAsp-----SerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThr 218
                                                                                                                                                                                                                                                                                                     ------TGTGGATAT 879
                                                                                                                                                                                                                                                                                                                                                                   880 ATAAATAGACTATATGTTCAATATTATCACTGCACTTATAAACAAAGAATGATATGTGAG 939
                    APPLICANT: Sawamura, Tatsuya
APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: McAulay Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/809,494A
FILING DATE: 24-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        259 ArgArgAlaGlyMetValLys 265
                                                                                                                                                                                                                                                                                                                                                                                                                                     940 AAGATGĠĊĊAATCCAĠTĠCAG 960
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Patent No. 5962260
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEPAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24408
                                                                                                                                                                                                                                                                                                     AATAACATGTAT-----
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REGISTRATION NUMBER: 244
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1897 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: New
STATE: NY
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US-08-809-494A-1
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------LysAlaGlyAlaHis 132
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383 ---ATGGAACTICACCGCCAGAACCTGAATCTCCAAGAAGTTCTGAAAAGAGGCAGCAAAC 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          203 TCCCAGGTCTCTGATCTCATAAAGAAACAGCAAGCAAATATTACTCACCAGGAAGATATT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 ------BrgLeuGlyAsnThrSerGlnGluLeuGlnSer 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 ProGluProArgArgThrGluHisArgAlaProSerSerThrTrpArgProValAlaLeu 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ThrieuLeuThrieuCysleuValLeuLeuIleGlyLeuAlaAlaLeuGlyLeuLeuPhe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 PheGlnTyrTyrGlnLeuSerAsnThrGlyGlnAspThrIleSerGlnMetGluGlu---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1897
80
41
111
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-689-742-160 (1-280) x US-08-809-494A-1 (1-1897)
                                                                                                                   LIBRARY: Bovine aortic endothelial cell cDNA CLONE: pBLOX-1
                                                                                                                                                                                                                                                             LOCATION: 1859...1864
OTHER INFORMATION: /function= "PolyA Signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
                                                         ORGANISM: Bos taurus
TISSUE TYPE: Vascular endothelial cells
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47.08%
31.13%
20.46%
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1880..1897
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1859..186
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                                                                          TISSUE TYPE: VEIMMEDIATE SOURCE:
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Query Match:
HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                               NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                          NAME/KEY:
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LOCATION:
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NAME/KEY:
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US-08-809-494A-1
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Pred. No.:
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PheTyrSerTyrTrpThrGlyLeuLeuArgProAspSerGlyLysAlaTrpLeuTrpMet 212
                   AspGlyThrProPheThrSerGluLeuPheHisIle-----IleIleAspValThrSer 230
                                                                                                       737 CCT---TCAGGGACCTGTGCATATATTCAAAGGGGAACTGTTTTTGCTGAAAACTGCATT 793
                                                                                                                                             231 ProArgSerArgAspCysValAlaileLeuAsnGlyMetIlePheSerLysAspCysLys
                                                                                                                                                                                                                    251 GluLeuLysArgCysValCysGluArgArgAlaGlyMetValLysProGlu 267
                                                                                                                                                                                                                                                        794 TTAACTGCATTCAGTATATGTCAAAAGAAGCGAATCTATTGAGAGCACAG 844
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Sawamura, Tatsuya
APPLICANT: Sawamura, Totsuya
APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: McAulay Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
STRIE: NY
STRIE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352,302
FILING DATE: 12-UUL-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY: Bovine aortic endothelial cell cDNA
CLONE: pBLOX-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Bos taurus
TISSUE TYPE: Vascular endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules B
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-436
TELECHONE: 212 986-4090
TELEPAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1897 base pairs
                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09352302
Patent No. 6197937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 10016-2391
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: polyA site LOCATION: 1880.71897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10016-2391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
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US-09-352-302-1
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500 TCTGGCTCTTTTAATTGGGAAAAAAGCCAGGAGAACTGCTTGTTTTGGATGCCCACTTG 559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             560 crcaacarraaraccacacacacacacrccaarrc---arccaccaarcarrcccarrcc 616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 ACTCTAGGGGTCCTTTGTCTGGGATTACTGGTGACTGTTATATTGTTGATACTGCAATTA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92 ------GinGluLeuGlyAsnThrSerGluLeuGlnSer 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 LeuGlnValGlnAsnileLys---LeuAlaGlySerLeuGlnHisValAlaGluLysLeu 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323 GAACTCAAAGAAATGATAGAAACCCTTGCCCACAAGCTGGATGAGAAATCCAAGAACTA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 CysArgGluLeuTyrAsn------132 CysArgGluLeuTyrAsalaHis 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 ---ATGGAACTTCACCGCCAGAACCTGAATCTCCAAGAAGTTCTGAAAGAGGCGAGCAAAC 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 ArgCysSerProCysThrGluGlnTrpLysTrpHisGlyAspAsnCysTyrGlnPheTyr 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             440 TATTCAGGTCCTTGTCCCCAAGACTGGCTCTGGCATGAAGAAACTGTTACCAATTTTCC 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153 LysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSerThrMet 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 PheTyrSerTyrTrpThrGlyLeuLeuArgProAspSerGlyLysAlaTrpLeuTrpMet 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 ProArgSerArgAspCysValAlalleLeuAsnGlyMetIlePheSerLysAspCysLys 250
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80
41
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25
CALION: 1859.1864
COTHER INFORMATION: /function= "Polya Signal"
FRATURE:
NAME/KEY: 5'UTR
LOCATION: 1.34
FRATURE:
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Matches:
Conservative:
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Indels:
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47.08%
31.13%
20.46%
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
FEATURE:
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; LOCATION:
US-09-352-302-1
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251 GluLeuLysArgCysValCysGluArgArgAlaGlyMetValLysProGlu 267
                                             Sequence 3, Application US/08809494A

Patent No. 5962260

GENERAL INFORMATION:
APPLICANT: Sawamura, Tatsuya
APPLICANT: Masaki, Tomoo

TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:
ADDRESSE: McAulay Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
BLILCATION NUMBER: US/08/809,494A
FILING DATE: 24-MAR-1997
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TISSUE TYPE: Vascular endothelial cells
IMMEDIATE SOURCE:
LIBRARY: Bovine aortic edothelial cells CDNA
CLONE: pBLOX-1
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LOCATION: 1864..1873
OTHER INFORMATION: /function= "PolyA Signal"
PRATURE:
NAME/KEY: 5'UTR
LOCATION: 1..34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JG-YY-4363PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIPICATION: 435
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: GOIGHOERY, Jules E
REGISTRATION NUMBER: 24408
REGISTRATION NUMBER: JG-YY-43;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TYPE: NUCLEIC acid
STRANDEDNESS: single
TOTAL SEGUENCE CHARACTERISTICS:
TOTAL SEGUENCE CHARACTERISTICS:
TOTAL SEGUENCE CHARACTERISTICS:
TYPE: NUCLEIC acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10016-2391
COMPUTER READABLE FORM:
MEDIUM TYPE: FIPOPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polyA_site
1889..1906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3' UTR
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ORIGINAL SOURCE:
ORGANISM: BOB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SES
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NAME/KEY:
LOCATION:
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LOCATION:
FEATURE:
NAME/KEY:
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362 CACAAGCTGGATGAGAAATCCAAGAAACTA---ATGGAACTTCACCGCCAGAACCTGAAT 418
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242 CAAGCAAATTTACTCACCAGGAAGATATCCTGGAGGACAGATTTTAGCCCAGCGCCGA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 LeuGlyAsnThrSerGlnGluLeuGlnSerLeuGlnValGlnAsnIleLys---LeuAla 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 GlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTyrAsn----- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 TyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAspLeuGlu 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           716 AGAÁTTCAGGGAGCTGTTTCCCGTATGTATCT---TCAGGGACCTGTGCATATTCAA 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 AsnGlyMetIlePheSerLyBAspCysLysGluLeuLyBArgCysValCysGluArgArg 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 TrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAspCysLys 162
                                                                                                                                                                                                                                                                                                                                                                                               92
                                                                                                                                                                                                                                                                                                         63 IleGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThrGly 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 ProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGluLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 SerThrTrpArg-----ProValAlaLeuThrLeuLeuThrLeuCysLeuValLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                             83 GlnAspThrileSerGlnMetGluGlu------Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09352302;
Patent No. 6197937;
GENERAL INPORMATION:
APPLICANT: Sawamura, Tatsuya
APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
                  1906
80
40
100
27
                                                             Conservative:
Mismatches:
Indels:
                                                                                                                                                                          US-10-689-742-160 (1-280) x US-08-809-494A-3 (1-1906)
                      Length:
Matches:
                                                                                                                                 Gaps:
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48.58%
32.39%
20.46%
                      1e-27
                                                               Percent Similarity:
Best Local Similarity:
Alignment Scores:
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                                                                                                        Query Match
                                             Score:
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1906
80
40
100
27
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352,302
FILING DATE: 12-JUL-1999
CLASSIFICATION:
                    NUMBER OF SEQUENCES: 8
CORRESPONDENCES. 8
CARRESPONDENCES. ADDRESSER: ACAULARY Fisher Nissen Goldberg & Kiel STREET: 261 Madison Avenue
STREET: NY
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
TISSUE TYPE: Vascular endothelial cells
IMMEDIATE SOURCE:
LIBRARY: Bovine aortic edothelial cells cDNA
CLONE: pBLOX-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
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LOCATION: 1889.71906
FRATURE:
NAME/KEY: misc RNA
LOCATION: 18647.1873
OTHER INFORMATION: /function= "PolyA Signal"
NAME/KEY: 5'UTR
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-00V-1994
PRIOR APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-70L-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
TELEPHONE: 212 986-4090
TELEPHONE: 212 986-4090
TELEPHONE: 212 986-4090
TELEPHONE: 212 986-4090
TELEPHONE: 212 889-479
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1906 base pairs
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Matches:
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FITLE OF INVENTION: Receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             308.50
48.58%
32.39%
20.46%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  857..1906
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Best Local Similarity:
Query Match:
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FEATURE:
NAME/KEY:
LOCATION:
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
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US-09-352-302-3
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                                                                                                              93 LeuGlyAsnThrSerGlnGluLeuGlnSerLeuGlnValGlnAsnIleLys---LeuAla 111
                                                                                                                                                                                                                                                                                        302 TCAGAAAATCTGCCCAGGAGTCACAGAAGGAACTCAAAAGAAATGATGAAACCCTTGCC 361
                                                                                                                                                                                                                                                                                                                                                    112 GlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTyrAsn----- 127
                                                                                                                                                                                                                                                                                                                                                                                              362 CACAAGCTGGATGAGAAATCCAAGAACTA---ATGGAACTTCACCGCCAGAACCTGAAT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                         128 -------iysAlaGlyAlaHisArgCysSerProCysThrGluGlnTrpLys 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - 143 TrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAspCysLys 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          539 GAGAACTGCTTGTTTTTGGATGCCCACTTGCTGAAGATTAATAGCACAGATGAACTGGAA 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 PheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeuLeuArg 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 Hisile-----IlelleAspValThrSerProArgSerArgAspCysValAlaileLeu 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg 260
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242 CAAGCAAATATTACTCACCAGGAAGATATCCTGGAGGGACAGATTTTAGCCCAGCGCGA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 CTCCAAGAAGTTCTGAAAGAGGCAGCAACTATTCAGGTCCTTGTCCCCAAGACTGGCTC 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    716 AGAÀTTCAGGGAGCTGTTTCCCGTATGTATCCT---TCAGGGACCTGTGCATATTTCAA 772
                                                                                  63 IleGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThrGly 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               656 AGGAAACCCAATTACTCGTGGCTTTGGGAAGATGGTACTCCTTTGACGCCCCACTTGTTT
                                                                                                                                                                 83 GlnAspThrIleSerGlnMetGluGlu-----Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 TyrPheCysleuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAspLeuGlu
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Patent No. 5962260
GENERAL INFORMATION:
APPLICANT: Sawamura, Tatsuya
APPLICANT: Masski, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
TITLE OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: MCAULARY Fisher Nissen Goldberg & Kiel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 AlaGlyMetValLysProGlu 267
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|||| GCGAATCTATTGAGAGCACAG 853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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10016-2391
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US-08-809-494A-5
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US-10-689-742-160 (1-280) x US-09-352-302-3 (1-1906)

771

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460 AAGCTGAATGAGAAATCCAAAGAGCAAATGGAACTTCACCACCAGAATCTGAATCTCCAA 519
                                                                                                                                                                     541 ---AATTGTTCAGCTCCTTGTCCGCAAGACTGGATCTGGCATGGAGAAAACTGTTACCTA 597
                                                                                                                                                                                                                                       151 PheTyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSer 170
                                                                                                                                                                                                                                                                  190 SerGluPhePheTyrSerTyrTrpThrGlyLeuLeuArgProAspSerGlyLysAlaTrp 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 LeuTrpMetAspGlyThrProPheThrSerGluLeuPheHisIle-----IleIleAsp 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 GlySerLeuGlnHisValAlaGluLysLeuCysArgGluLeuTyrAsnLysAlaGlyAla 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 ValThrSerProArgSerArgAspCysValAlaIleLeuAsnGlyMetIlePheSerLys 247
                                                                                                                                        132 HisArgCysSer---ProCysThrGluGlnTrpLysTrpHisGlyAspAsnCysTyrGln
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                                                                                                                                                                                                                                                                                                                               171 ThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaAlaSerGln---SerTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 AspCysLysGluLeuLysArgCysValCysGluArgArgAlaGlyMet 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         889 AACTGCATTTTAGCTGCCTTCAGTATATGTCAGAAGAAGGCAAACCTA 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-352-302-5
US-09-352-302-5
Patent No. 6137937
Patent No. 6137937
GENERAL INFORMATION:
APPLICANT: Sawamura, Tatsuya
APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCAULAY Fisher Nissen Goldberg & Kiel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: 10016-2391
COMPUTER: Floppy disk
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC COMPONIAN
SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352,302
FLING DATE: 12-JUL-1999
CLASSIFICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTONIVEY/AGENT INPOMMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24408
REGISTRATION NUMBER: 24408
REGISTRATION NUMBER: 24408
TELEBPHONE: 212 986-4090
                                                                                            520 GAAACACTGAAGAGAGTAGCA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 261 Madison Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 212 818-9479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 10016-2391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         340 GCAAACCTAACTCACCAGAAAAAGAAACTGGAGGGACAGATCTCAGCCCGGCAACAAGCA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 SerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeuLeulle 63
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         CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/809,494A

FILING DATE: 24 MAR.1997

CLASSIPICATION NUMBER: US/08/809,494A

FILING DATE: 30 NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: D6-321705

FILING DATE: 30 NOV-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: D7-214206

FILING DATE: 31-UL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Goldberg, Jules E

REGISTRATION NUMBER: 24408

REGISTRATION NUMBER: 24408

REGISTRATION NUMBER: 24408

REFERENCE/DOCKET NUMBER: JG-YY-4363PCT

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: 212 818-9479

INFORMATION FOR EQ ID NO: 5:

SEQUENCE CRARACTERISTICS:

LENGTH: 1318 base pairs

STRANDESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-689-742-160 (1-280) x US-08-809-494A-5 (1-1318)
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE TYPE: Lung, placenta
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIBRARY: Human lung cDNA CLONE: lambdahLOX-1 FEATURE: NAME/KEY: 5'UTR
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42.97%
29.30%
19.99%
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66..125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
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LOCATION:
FEATURE:
NAME/KEY:
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US-08-809-494A-5
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APPLICANT: Ariizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
CORRESPONDENCES: 42
CORRESPONDENCE ADDRESS:
   ||| || || || || CCAGTTCTGGATGGGGCTGTCTCGGAGGAGCCCCAGCTACCCATGG 771
                                                                                                210 LeuTrpMetAspGlyThrProPheThrSerGluLeuPheHisIle-----IleIleAsp 227
                                                                                                                                                          772 cicidegaggacicircicirroargccccacirariragagrccgaggcgcrcrcrcc 831
                                                                                                                                                                                                              * 228 ValīḥrSerproArgSerArgAspCysValAlaileleuAsnGlyMetllePheSerLys 247
                                                                                                                                                                                                                                                           LysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMetSerLeuHis 23
                                                                                                                                                                                                                                                                                                                                                                                  248 AspCysLysGluLeuLysArgCysValCysGluArgArgAlaGlyMet 263
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
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/note= "Y = C or T"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/08772440 ; Patent No. 6046158
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TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,1
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.54e-25
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STRANDEDNESS: single
TOPOLOGY: linear
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OTHER INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 HisArgCysSer---ProCysThrGluGlnTrpLysTrpHisGlyAspAsnCysTyrGln 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 GAAGAAGCTTCACAGGAGTCAGAAAACGAACTCAAGGAAATGATAGAAACCCTTGCTCGG 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 ArgleuGlyAsnThrSerGlnGluLeuGlnSerLeuGlnValGlnAsnIleLysLeuAla 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 PheTyrLysAspSerLysSerTrpGluAspCysLysTyrPheCysLeuSerGluAsnSer 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190 SerGluPhePheTyrSerTyrTrpThrGlyLeuLeuArgProAspSerGlyLysAlaTrp 209
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Matches:
Conservative:
Mismatches:
Indels:
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TISSUE TYPE: Lung, placenta
IMMEDIATE SOURCE:
LIBRARY: Human lung CDNA
CLONE: lambdahLOX-1
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| 520 GAACACTGAAGAGAGTAGCA
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                                                          LENGTH: 1318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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42.97%
29.30%
19.99%
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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949..1309
                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
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127..948
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LOCATION: 66..125
FEATURE:
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Best Local Similarity:
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DB:
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                                                             122 CysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGlnTrp 141
                                                                                                                                                                                                                                                                                                                                              398 GCTCCCTCCAAGGCATCCCAAACTACAGGAGGTTTTTCTCAGTCTTGCCTTCCTAATTGG 457
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                                                                                                                                                                                                                                                                                                                                                                        142 LysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAspCys 161
                                                                                                                                                                                                                                                                                                                                                                                                                             LysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAspLeu 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                      518 AAGAGACACTGCTCCCAGCTAGGTGCTCATCTACTGAAGATAGACAACTCAAAAGAATTT 577
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                                                                                               AlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeu 61
                                                                                                                                                     LeulleGlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThr 81
                                         SerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGlu-----HisArg
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Patent No. 5932445
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Reddy, Roopa
APPLICANT: Marry, Lynn E.
APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE - C
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 Tyr-AsnLysAlaGly--------AlaHisArgCysSerProCysThrGl 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310 GTAAAACAATCAGAACTAAAAGGGCACTTTCAAAGGTCATAAATGCAGCCCTGTGAACAC 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 SerThrArgAsp --- MetLeuAspAspAspGlyAspThrThrMetSerLeuHisSerGln 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 ThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeuLeuIleGlyLeu 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 AlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThrGlyGlnAspThr 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 AAACCAĞCTCTCGTC--------TCCGTTGGCCCTGCATCCTCCTC
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Mismatches:
Indels:
                                                                                                            OPERATING SYSTEM: DOS CORRESTING SYSTEM: DOS CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/966,316 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: ATTORNEY APPLICATION NUMBER: ATTORNEY AGENT INFORMATION: NAME: Billings, Lucy J. NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-689-742-160 (1-280) x US-08-966-316-15 (1-617)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                       E: Diskette
IBM Compatible
SYSTEM: DOS
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277.00
50.22$
30.40$
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
LENGTH: 617 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 650-845-4166
COMPUTER READABLE FORM MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                179 uAspLeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGl 199
                                                                                                                                         199 yLeuLeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSe 219
                           159 uAspCysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGl 179
                                              |::: |||| |:: ::|||
430 AGAGAGTAAGCAGTACTGCACTGACATGAATGCTACTCCTGCAAGATTGACAACCGGAA 489
                                                                                                            490 CATTGTGGAGTACAT-CAAAGCCAG-----GACTCATTTAATTCGTT-TGGGTCNG 538
370 AAACTGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACTTAACATGGGA 429
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70
28
101
62
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-689-742-160 (1-280) x US-08-688-342-2 (1-990)
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,342
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               Sequence 2, Application US/08688342 Patent No. 5871964
                                                                                                                                                                                                219 rGluLeuPheHisIlelle 225
                                                                                                                                                                                                                   599 AAATATGNTTGAGTTTTTG 617
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
MEDIUM TYPE: Diskette
THE COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmac
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELERAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 990 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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37.55%
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Best Local Similarity:
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Pred. No.:
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84 AspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGlnSerLeu 103
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                                                                                                                                                                                                                                     132 TTCGACTCTCAAAGCAATACCAGGATAGCTGTTTTCAGAGAAAGGATCGTGTGCTGCA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 GlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLysLeuCysArg 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 GluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGlnTrpLysTrp 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                315 TATGAGAAGAGCTGTTATCTATTCAGCATGTCACTAAATTCCTGGGATGGAAGTAAAAGA 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 PheCysleuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAspLeuGluPhe 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375 caardcregcaacreggcricraarcrecraaagaragacagcreaaargaarrigggarrir 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   435 ATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTTGGATAGGCCTTTCTCGGCCC 494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 AspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGluLeuPheHis 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224 ilelleleAspValThrSerProArg---SerArgAspCysValAlaileLeuAsnGly 242
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                                                                                                                                                        24 SerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHisArgAlaPro
4 LysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMetSerLeuHis
                                                                                                                                                                                                                                                                                                                          SerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeuLeuIle
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US-09-746-783-159
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-MODEL=frame+ pln.model -DEV=xlp
-MODEL=frame+ pln.model -DEV=xlp
-G-Cgn2 1/USPTO_spool p/US10689742/runat_07102005_183119_28021/app_query.fasta_1.718
-G-Cgn2 1/USPTO_spool p/US10689742/runat_07102005_183119_28021/app_query.fasta_1.718
-DB-Published Applications NA -OFWT=fastap -SUFFTX=pln.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS-bluman40.cdi -LIST=45 -DOCALIGN=200 -THR MXX=EDC -THR MXX=EDC -THR MXX=EDC -THR MXX=CDC -DOCALIGN=15 -MODE=LOCAL -OUTFWT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10689742 @CGN i 1 879 @runat 07102005 183119_28021
-NCPU-6 -ICVU-3 -NO MANAP -LARGEQUERY NEG SCORESSO -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMBOTT=120 -WARN TIMBOTT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                          // Search time 921.136 Seconds
(without alignments)
2117.119 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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10: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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- 2005 Compugen Ltd.
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Ygapop 10.0,
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 318, Assequence 318, 
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Sequence 31
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US-09-989-727-318
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; GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
В
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APPLICANT: Zhang, Zemin TITIEN APPLICANT: Zhang, Zemin TITIEN OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITIE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITIE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2/30PLG3
CURRENT PILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-06-17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-14
PRIOR PILING DATE: 1998-02-25
549 TGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGATAAACAACAAGAAGA
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; Patent No. US200220072067Al
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
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Gurney,Austin L.
Kljavin,Ivar J.
Napier,Mary A.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleone
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Gerber, Hanspeter
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Godowski, Paul
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                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPTAING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: «Unknown>
ATTORNEY/ACGNT INFORMATION:
NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELEPHONE: (617) 742-4214
INFORMATION: (617) 742-4214
INFORMATION: (617) 742-4214
INFORMATION: CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Matches:
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DESCRIPTION: /desc = "oligonucleotide"

SEQUENCE DESCRIPTION: SEQ ID NO: 159:
US-09-746-783-159
                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
COUNTRY: U.S.A.
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Best Local Similarity:
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Pred. No.:
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PRIOR PLING DATE: 1998-06-19

PRIOR PLING DATE: 1998-06-12

PRIOR PLING DATE: 1998-06-13

PRIOR PLING DATE: 1998-06-14

PRIOR PLING DATE: 1998-06-15

PRIOR

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APPLICANT: ROY, Margare Ann Applicants F. APPLICANT: ROY, Margare Ann APPLICANT: Story A Margare Ann APPLICANT: Story A Margare Ann APPLICANT: Story Edwart, Timed by APPLICANT: Tumas, Daniel APPLICANT: Tumas, Daniel APPLICANT: Williams P. Mickey APPLICANT: Williams P. Mickey Edwart: Williams P. Mickey Edwart: Williams P. Mickey Edwart: Tring OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Title OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Title OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Title OF INVENTION: 2010-11.13

PRIOR PEDICATION NUMBER: 06/04999

PRIOR PLING DATE: 1990-06-15

PRIOR PEDICATION NUMBER: 06/06510

PRIOR PEDICATION NUMBER: 06/06511

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PRIOR PEDICATION NUMBER: 06/06106

PRIOR PEDICATION NUMBER: 06/08100

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PRIOR PEDICATION NUMBER: 06/081609

                       261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp
                                                                                                                         ; Sequence 318, Application US/09989723; Patent No. US20020072092A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Fong, Sherman
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Napier, Mary A.
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Botstein, David
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                                                                                                        US-09-989-723-318
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Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR PILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
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DATE	DATE	APPLICATION FILING DATE	TION	LING DATE	FILING DATE	DATE	TION	APPLICATION FILTING DATE	PPLICATION	FILING DATE:	NG DATE	APPLICATION FILING DATE:	PPLICATION	APPLICATION		DATE	NOIT	PLICATION	FILING DATE:	CATION 3 DATE	ATION	FILING DATE: APPLICATION	DATE	DATE	PPLICATION	A.	FILING DATE:	FILING DATE:	APPLICATION FILING DATE:	TION	ATION	LION	DATE	DATE	DATE	APPLICATION FILING DATE:	PPLICA	FILING DATE:	ILING	APPLICATION FILTING DATE	PPLICA	LING	ILING DA	PPLICATION	PPLICATI	FILING DATE:
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PRIOR PAPLICATION NUMBER: 60/090349
PRIOR PILING DATE: 1998-06-23
PRIOR PILING DATE: 1998-06-24
PRIOR PILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR PAPLICATION NUMBER: 60/090435
PRIOR PELING DATE: 1998-06-24
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-26
PRIOR PELING DATE: 1998-07-07
PRIOR PELING Alignment Scores: Pred. No.:

US-10-689-742-160 (1-280) x US-09-989-723-318 (1-1841) Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:

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Percent Similarity: Best Local Similarity: Query, Match: DB:

Score:

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1 MetGlnalaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet 20

Napier,Mary A. Pan,James Paoni,Nicholas F. Roy, Margaret Ann Stewart, Timothy A.

Tumas, Daniel

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PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-06-28
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PRIOR PILING DATE: 1998-06-28
PRIOR PILING DATE: 1998-06-07
PRIOR APPLICATION NUMBER: 60/08852
PRIOR PILING DATE: 1998-06-07
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APPLICATION NUMBER: 60/089514
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APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/089440
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APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Calin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: And Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLG5
CURRENT APPLICATION NUMBER: US/09/989,727
CURRENT FILIAGO DATE: 2001-11-19
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PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-111-12
PRIOR FILING DATE: 1997-11-13
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Gurney,Austin L.
Kljavin,Ivar J.
Napier,Mary A.
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Goddard, Audrey
Godowski, Paul J.
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Gerber, Hanspeter
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PRIOR APPLICATION NUMBER: 60/088026
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PRIOR PELING DATE: 1998-06-05
PRIOR PELING DATE: 1998-06-10
PRIOR PELING DATE: 1998-06-11
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PRIOR PELING DATE: 1998-06-17

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R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/089948
R FILING DATE: 1998-06-19
R APPLICATION NUMBER: 60/08952
R FILING DATE: 1998-06-19
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APPLICATION UNMBER: 60/089907
FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089908
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APPLICANT: Stewart, Timoth A.
APPLICANT: Stewart, Timoth A.
APPLICANT: Tunas, Daniel
APPLICANT: William I.
APPLICANT: William P. Mickey
APPLICANT: Walliam P. Mickey
APPLICANT: Anod, William I.
APPLICANT: Zhang, Zemin
TITLE OF INWENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PL70
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/06230
PRIOR PLILNG DATE: 1997-01-17
PRIOR PLILNG DATE: 1997-11-12
PRIOR PLILNG DATE: 1997-11-12
PRIOR PLILNG DATE: 1997-11-12
PRIOR PLILNG DATE: 1997-11-12
PRIOR PLILNG DATE: 1997-11-24
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PRIOR PLILNG DATE: 1998-03-20
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PRIOR PLILNG DATE: 1998-04-28
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PRIOR PLILNG DATE: 1998-06-22
PRIOR PLILNG DATE: 1998-06-22
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PRIOR PLILNG DATE: 1998-06-03
PRIOR PLILNG DATE: 1998-06-03
PRIOR PLILNG DATE: 1998-06-03
PRIOR PLING DATE: 1998-06-03
                                     261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
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241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg
                                                                                                                                                                                                                                                                                                 Sequence 318, Application US/09989731
Patent No. US20020103125A1
GENERAL INFORMATION:
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
Pan, James
Paoni, Nicholas F.
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FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
APPLICATION NUMBER: 60/088025
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Stewart, Timothy A.
Tumas, Daniel
Watanabe, Colin K.
Williams, P. Mickey
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Fong, Sherman
Gerber, Hanspeter
Gerritesn, Mary E.
Goddard, Audrey
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                                                                                                                                      204 AGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGCGCACAGAGCAC
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                                     MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet
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US-10-689-742-160 (1-280) x US-09-989-731-318 (1-1841)
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
APPLICANT: Besnoyers, Luc
APPLICANT: Perrara, Napoleone
APPLICANT: Ferry Seno, Sheman
APPLICANT: Ferry Seno, Sheman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerittsen, Mary E.
APPLICANT: Geritsen, Mary E.
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PRIOR APPLICATION NUMBER: 60/08812
PRIOR PLING DATE: 1998-66-10
PRIOR APPLICATION NUMBER: 60/08824
PRIOR APPLICATION NUMBER: 60/08826
PRIOR APPLICATION NUMBER: 60/08826
PRIOR APPLICATION NUMBER: 60/08826
PRIOR APPLICATION NUMBER: 60/08861
PRIOR PLING DATE: 1998-66-11
PRIOR PLING DATE: 1998-66-10
PRIOR APPLICATION NUMBER: 60/090429
PRIOR PLING DATE: 1998-66-20
PRIOR APPLICATION NUMBER: 60/090431
PRIOR PLING DATE: 1998-66-20
PRIOR PLING DATE: 1998-6
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090535
APPLICATION NUMBER: 60/088734
                                              1998-06-
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APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2130PIG57
CURRENT APPLICATION NUMBER: US/09/989,732
CURRENT FILING DATE: 2001-11-19
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PRIOR APPLICATION NUMBER: 60/062260
PRIOR APPLICATION NUMBER: 60/06216
PRIOR PILING DATE: 1997-01-17
PRIOR PELICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-12
PRIOR PILING DATE: 1997-11-13
PRIOR PILING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-24
PRIOR PELING DATE: 1998-01-25
PRIOR PELING DATE: 1998-04-28
PRIOR PELING DATE: 1998-06-07
PRIOR PELING DATE: 1998-06-06-07
PRIOR PELING DATE: 1998-06-06-07
PRIOR PELING DATE: 1998-06-06-07
PRIOR PELING DATE: 1998-06-06-07
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R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088217
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/088655
R FILING DATE: 1998-06-09
                                          Grimaldi,J.Christopher
Gurney,Austin L.
Kljavin,Ivar J.
                                                                                                                                                                        Napier, Mary A.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timcthy A.
Tumas, Daniel
Godowski, Paul J.
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APPLICANT:
APPLICANT:
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APPLICANT: Grimeldi, J. Christopher
APPLICANT: Grimeldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William; P. Mickey
APPLICANT: Wood, William; D. Mickey
APPLICANT: Scarreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC15
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             CAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA
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Sequence 318, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
Napier, Mary A.
Pan, James
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-62-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Eaton, Dan L.
Ferrara, Napoleone
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APPLICANT: Baker, Kevin P.
APPLICANT: Betsetin, David
APPLICANT: Benoyers, Luc
APPLICANT: Perrara, Napoleone
APPLICANT: Perrara, Napoleone
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gedowski, Paul J.
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Conservative:
Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: 60/090540
PRIOR PILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/09057
PRIOR PLING DATE: 1998-06-25
PRIOR PELING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR PELING DATE: 1998-06-25
PRIOR PELING DATE: 1998-07-01
PRIOR PELING DATE: 1998-07-02
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864 AATGGGATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTGTCTGTGAGAGAGG
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       221 LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu
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                          Gerber, Hanspeter
Gerritsen, Mary E.
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Patent No. US2002013253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Bestein, David
APPLICANT: Eaton, Dan L.
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US-10-689-742-160 (1-280) x US-09-991-163-318 (1-1841)

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PRIOR APPLICATION NUMBER: 60/065111
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  TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp 160
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                                                                                              CTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGACAGGGCTT
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APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC25
CURRENT APPLICATION NUMBER: 105/09/993,604
CURRENT FILING DATE: 2001-11-14
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Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Baker.Kevin P.
APPLICANT: Boterin, David
APPLICANT: Boterin, David
APPLICANT: Boterin, David
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone.
APPLICANT: Ferrara, Napoleone.
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Ginmaldi, John:
APPLICANT: Grimaldi, John:
APPLICANT: Kljavin, Ivar J.
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Gurney,Austin L.
Kljavin,Ivar J.
Napier,Mary A.
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Wood, William I.
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Stewart, Timothy A.
Tumas, Daniel
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Paoni, Nicholas F.
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1998-06-12 NUMBER: 60/089440 1998-06-16 1998-06-16 1998-06-16 1098-06-16 1098-06-16 NUMBER: 60/089514 1998-06-17 1998-06-17 NUMBER: 60/089538 1998-06-17 NUMBER: 60/08959	1998 - NUMBER NUMBER NUMBER NUMBER 1998 - NUMBER 1998 - NUMBER NUMBER 1998 - NUMBER NUMBER NUMBER NUMBER 1998 - NUMBER 1998 - 1998 - NUMBER 1998 - 1998 - NUMBER 1998 - 1998 - NUMBER NU	NUMBER: 60/090445 1998-06-24 1998-06-24 1998-06-24 NUMBER: 60/090535 1998-06-24 NUMBER: 60/090542 1998-06-24 1998-06-24 1998-06-24 1998-06-24 1998-06-25 NUMBER: 60/090676 1998-06-25 NUMBER: 60/090676 1998-06-25 NUMBER: 60/090678 1998-06-25 NUMBER: 60/090690 1998-06-25 NUMBER: 60/090690 1998-06-25 NUMBER: 60/090690 1998-06-25 NUMBER: 60/090690 1998-06-25 NUMBER: 60/090695 1998-06-25 NUMBER: 60/090695
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PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08759
PRIOR APPLICATION NUMBER: 60/08021
PRIOR FILING DATE: 1998-06-03
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR PLILING DATE: 1998-06-07
PRIOR PLILING DATE: 1998-06-05
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PRIOR PLILING DATE: 1998-06-11
PRIOR PLILING DATE: 1998-06-12
PRIOR PLILING DATE: 1998-06-12
PRIOR PLILING DATE: 1998-06-17
PRIOR PLILING DATE: 1998-06-
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C22
CURRENT APPLICATION NUMBER: US/09/990,456
CURRENT FILING DATE: 1997-01-11-14
RIOR APPLICATION NUMBER: 60/06226
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/06570
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/06570
PRIOR PILING DATE: 1998-04-28
PRIOR PILING DATE: 1998-05-06-28
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     LeuårgProåspSerGlyLysalaTrpLeuTrpMetaspGlyThrProPheThrSerGlu 220
                                   804 CTGTTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTC 863
                                                                                                                                                                                                                               261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp 280
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                                                                                                 LeuPheHisIleIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu
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US-09-990-456-318

i Sequence 318, Application US/0990456
; Patent No. US20020137890A1
; GENERAL INFORMATION:
    APPLICANT: Ashkenazi, Avi J.
    APPLICANT: Baker, Kevin P.
    noritCANT: Botstein, David
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FILING DATE: 1998-06-02
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Grimaldi, J. Christopher
Gurney, Austin L.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Pan, James
Paoni, Nicholas F.
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Eaton, Dan L.
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NUMBER: 60/089908 1998-06-18 NUMBER: 60/089947 1998-06-19 NUMBER: 60/08952 1998-06-19 NUMBER: 60/08952 1998-06-2 NUMBER: 60/090246 1998-06-22 1998-06-22 NUMBER: 60/090252 1998-06-22 NUMBER: 60/090252 1998-06-22 NUMBER: 60/090252	NUMBER: 60/090349 NUMBER: 60/090355 NUMBER: 60/090355 NUMBER: 60/090429 NUMBER: 60/090431 1998-06-24 NUMBER: 60/090444 1998-06-24 NUMBER: 60/090445 1998-06-24 NUMBER: 60/090445 1998-06-24 NUMBER: 60/090445 1998-06-24 NUMBER: 60/090557 NUMBER: 60/090540 1998-06-24 NUMBER: 60/090540 1998-06-24 NUMBER: 60/090540 1998-06-24 NUMBER: 60/0905678 1998-06-25 NUMBER: 60/090578 1998-06-25 NUMBER: 60/090578 1998-06-25 NUMBER: 60/090578 1998-06-25 NUMBER: 60/090578 NUMBER: 60/090578 NUMBER: 60/090578 NUMBER: 60/090678 NUMBER: 60/090678 NUMBER: 60/090678 NUMBER: 60/090678	NUMBER: 6 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-06-1 1998-07-1 1998-07-1 1998-07-1 1998-07-1 1998-07-1 1998-07-1 1998-07-1 1998-07-1 1998-07-1
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PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-05

PRIOR PILING DATE: 1998-06-05

PRIOR PILING DATE: 1998-06-05

PRIOR APPLICATION NUMBER: 60/08635

PRIOR APPLICATION NUMBER: 60/08634

PRIOR APPLICATION NUMBER: 60/08634

PRIOR PILING DATE: 1998-06-10

PRIOR PILING DATE: 1998-06-11

PRIOR PILING DATE: 1998-06-17

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CURRENT APPLICATION WUMBER: US/09/989,721
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-06-05
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Watanabe, Colin K.
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Stewart, Timothy A.
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APPLICANT: Walliams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Thang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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                                                                                                                                                                                                                                                   LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln
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Gurney,Austin L.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Bacon, Dan I.
APPLICANT: Ferrara, Napoleone
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Napier, Mary A.
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R FILING DATE: 1998-06-25

R APPLICATION NUMBER: 60/090690

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R APPLICATION NUMBER: 60/090694

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R APPLICATION NUMBER: 60/090695
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R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/091982
R FILING DATE: 1998-07-07
R APPLICATION NUMBER: 60/092182
R FILING DATE: 1998-07-09
                       R APPLICATION NUMBER: 60/090444
R FILING DATE: 1998-06-24
R APPLICATION NUMBER: 60/090445
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R FILING DATE: 1998-06-24
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R FILING DATE: 1998-06-26
R APPLICATION NUMBER: 60/091360
R FILING DATE: 1998-07-01
R APPLICATION NUMBER: 60/091478
R FILING DATE: 1998-07-02
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/090542
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FILING DATE: 1998-07-01
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FILING DATE: 1998-07-02
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APPLICANT: Anternazi, Avi J.
APPLICANT: Anternazi, Avi J.
APPLICANT: Anternazi, Avi J.
APPLICANT: Beaker, Kevin David
APPLICANT: Beaker, Kevin David
APPLICANT: Beenoyers, Inc.
APPLICANT: Beenoyers, Inc.
APPLICANT: Gerber, Hangelen
APPLICANT: Gerber, Hangelen
APPLICANT: Goddard, Andrey
APPLICANT: Gutney, Assistin L.
APPLICANT: Wajter, Mary A.
APPLICANT: Wajter, Mary B.
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                                      LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu
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PRIOR FILING DATE: 1999-06-25
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PRIOR APPLICATION NUMBER: 60/090863
PRIOR APPLICATION NUMBER: 60/091860
PRIOR PILING DATE: 1998-06-26
PRIOR PELING DATE: 1998-06-26
PRIOR PLING DATE: 1998-07-01
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PRIOR APPLICATION NUMBER: 60/091544
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PRIOR PLIKING DATE: 1998-06-25
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Search completed: October 8, 2005, 04:31:49 Job time : 930.136 secs

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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr-web: www.genoscope.cns.fr) and common the trand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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CB453572 709449 MA
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full-length cDNA clone CS0DI081YG24 of Placenta Cot 25-normalized
on Enno Sapiens (human).
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http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
                                                                                                       BX339075
BX380212
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Homo sapiens (human)
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Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1p
-MODEL=frame+ p2n.model -DEV=x1p
-MODEL=frame+ p2n.model -DEV=x1p
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-DEV=XD_1/USPTO_spool_p/US10689742/runat_07102005_183118_27976/app_query.fasta_1.718
-DEV=XD_1/USPTO_SEVENTE -END=-1 -MATRIX=DIOSUM62 -TEANS=human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TEANS=human40.cdi -LIST=45
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-NO_MMAP -LARREQUERY -NGS_SCORES=0 -MATT -DSPBALOCK=100 -LONGING
-DSW_TIMEOUT=120 -WARN_TIMEOUT=30 -THERADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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CR598502 full-leng
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                                                                                                                                                                                                                                                                                       1 MQAKYSSTRDMLDDDGDTTM.....AGMVKPESLHVPPETLGEGD 280
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Compugen Ltd
                                                                                                           nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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CR619172
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, Ygapext
, Fgapext
, Delext
                         GenCore (c) 1993
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Maximum DB seq length: 200000000
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Delop 6.0,
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Database :

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Genoscope.

Direct Submission

Submitted (20-UTL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 ENRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCNVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
                                      CR614400 1671 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0D1036YF20 of Placenta Cot 25-normalized
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                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1671)
1 ("H. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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                                                                                                                                                                                                                                                     Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fullength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/clone="CSODI036YF20"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
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HTC; CNSLT cDNA.
Homo sapiens (human)
Homo sapiens
                                                                     of Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                           345 CAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA 404
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                                                                                                                                                                                                                                                                                                                              CIGCIGATAGGGCIGGCAGCCCTGGGGCTTTTGTTTTTCAGTACTACCAGCTCTCCAAT
                                                                                                                                              1 MetGlnAlaLygTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet
                                                                                                                                                                                                                                                            ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1734 bp mRNA linear full-length cDNA clone CSODI049YB09 of Placenta Cot of Homo sapiens (human).
                       1692
279
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1
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                     Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                      US-10-689-742-160 (1-280) x CR591231
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Best Local Similarity:
Query Match:
DB:
Alignment Scores:
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR591231 1602 bp mRNA linear HTC 21-JUL-2004 full-length cDNA clone CS0DI041YA14 of Placenta Cot 25-normalized CF Homo sapiens (human).
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1 (bases 1 to 1692)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                                                                                                                                                                                                                                                                                                                                                         AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg
                        TGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAAAAAGTTGGGAC
                                                                                                                                                  TGTAAATATTTCTGCCTTAGTGAAAACTCTACCATGCTGAAGAAGAAAAACAAAGAAGAAGAC
                                                                                                                                                                                        LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu
                                                                                                                                                                                                      LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu
                                                                                                                                                                                                                                                                   TrpLysTrpHisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAsp
                                                                                                                                   CysLysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
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/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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HTC; CNSLT cDNA.
Homo sapiens (human)
Homo sapiens
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CR591231
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HTC 21-JUL-2004 25-normalized

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260

824

644

704

280

704

584 200 644 240 764 260 824 280

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 1045)

2. I (bases 1 to 1045)

3. Ii, W.B., Gruber, C., Jessee, J. and Polayes, D.

Pull-length cDNA libraries and normalization

4. Unpublished (2001)

On May 8, 2003 this sequence version replaced gi:30439428.

Contact: Genoscope

Centre National de Sequencage

2 rue daston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enrithed, double-erirand cDNA was dispested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BX379905

1045 bp mRNA linear EST 23-APR-2004
BX379905 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI041YA14 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     465 TGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGAC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-coligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
                                                                                                                                            LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu
                                                                                                                                                                            CTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTT
                                                                                                                                                                                                                                                                                645 TIGCGCCCTGACAGTGGCCTGGCCTGGATGGATGGAACCCCTTTCACTTCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                               241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg
                                                   CyslysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp
                                                                                               LeuArgProAspSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu
                                                                                                                                                                                                                                                                                                                                    LeuPheHisIleIleAspValThrSerProArgSerArgAspCysValAlaIleLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGluGlyAsp
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/db_xref="taxon:9606"
/clone="CSODI041YA14"
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Pred. No.:
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Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecox V sites of the pCMVgPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             285 ACTGGTCAAGACACCATTTCTCAAATGGAAGAATTAGGAAATACGTCCCAAGAGTTG 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 345 CAATCTCTTCAAGTCCAGAATATAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAA 404
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                                                                       Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                               Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Placenta_Cot_25-normalized"
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                                                                  Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Primates; Catarrhini; Hon
1 (bases 1 to 1734)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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Matches:
Conservative:
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/clone="CS0DI049YB09"
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1504.00
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99.64%
                           sapiens (human)
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                                                   Homo sapiens
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PheCysLeuSerGluAsnSerThrMetLeuLyslleAsnLysGlnGluAspLeuGluPhe
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 1673)
                  Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished
                                                                                                                                                                                                                                                                                                                                                        Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                           1. .1673
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODE006YK19"
/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                             Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCygLeuVal
                                                                                                                                                                          AGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGTGCTTGGTG
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                                                                                                                                                                                                                                                                                                                                             LeuCysArgGluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGln
                                                                                                                                                                                                                                                                                                                                                         TGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGAC
                                                                    MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet
                                                                                                                SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis
 Mismatches:
Indels:
Gaps:
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CR606141.1 GI:50486948
HTC; CNSLT_CDNA.
HOMO Sapiens (human)
Homo sapiens
                                            US-10-689-742-160 (1-280) x BX379905
 98.93%
98.94%
  Local Similarity:
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | 192 191 91006 EVRY sequence from en eriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Inviltogen. GlnValGlnAsnIleLysLeuAlaGlySerLeuGlnHisValAlaGluLysLeuCysArg 123 143 163 183 241 84 AspThrIleSerGlnMetGluGluArgLeuGlyAsnThrSerGlnGluLeuGlnSerLeu 103 301 361 481 62 TCTCAAGGCTCTGCCACAACTCGGCATCCAGAGCCCCGGGGGGCACAGAGCACAGGGCTCCC 121 63 181 421 61 43 83 44 SerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuValLeuLeuIle 122 TCTTCAACGTGGCGACCAGTGCCCTGACCCTGCTGACTTTGTGCTTGGTGCTGCTGATA 182 GGGCTGGCAGCCCTGGGGCTTTTTTTTTTTTACAGTACTACCAGCTCTCCAATACTGGTCAA 242 GACACCATTCTCAAATGGAAGAAAAGATTAGGAAATACGTCCCAAGAGTTGCAATCTCTT GluLeuTyrAsnLysAlaGlyAlaHisArgCysSerProCysThrGluGlnTrpLysTrp GAGCTGTATAACAAAGCTGGAGCACACACAGGTGCAGCCCTTGTACAGAACAATGGAAATGG HisGlyAspAsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAspCysLysTyr 4 LysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMetSerLeuHis SerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHisArgAlaPro GlyLeuAlaAlaLeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAsnThrGlyGln CAAGTCCAGAATATAAAAGCTTGCAGGAAGTCTGCAGCATGTGGCTGAAAAACTCTGTCGT Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue

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100 AGCCTGCATTCTCAAGGCTCTGCCACAACTCGGCATCCAGAGCCCCGGCGCGCACAGAGCAC 159
                                                                                                                                                                  160 AGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGCTGACTTTGTGTGCTTGGTG 219
                                                                                                                                                                                                                          280 GGATCCTGGTTCCAAGTTTTTCAGTACTACCAGCTCTCCAATACTGGTCAAGACACCATT 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 LysAspCysLysGluLeuLysArgCysValCysGluArgArgAlaGlyMetValLysPro 266
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1759)
SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis
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                                                                                                                               ArgAlaProSerSerThrTrpArgProValAlaLeuThrLeuLeuThrLeuCysLeuVal
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Submitted (20-JUJ-2004) Genoscope - Centre National de Sequencage :
BP 191 9100 GENY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
191 910 6ENY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
18t strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1747)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished
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                                                                                                          AlaalaSerGlnSerTyrSerGluBhePheTyrSerTyrTrpThrGlyLeuLeuArgPro
                                                                                                                                                                                 IlelleleAspValThrSerProArgSerArgAspCysValAlaileLeuAsnGlyMet
                                                                                                                                                                                                                        ATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTTAATGGGATG
                                                                                                                                                                                                                                                         IlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArgAlaGlyMet
GCCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGCTTTTTGCGCCCT
                                                                                                                                                                                                                                                                                                 ATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTGTCTGTGAGAGGGCAGGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
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HTC; CNSLT_cDNA.
Homo sapiens (human)
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Best Local Similarity:
Query Match:
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HTC 21-JUL-2004 25-normalized

Alignment Scores: Pred. No.:

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ORIGIN

168 GludenSerThrmetLeuLyelledshiysGludludepi 600 GabadrictataaaGacaGacacacacacacacacacacacacacac	9009 7 7 ES	KEYWORDS EST. SOURCE Home sapiens (human) ORGANISM Home sapiens (human) ORGANISM Home sapiens Ebraryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Home. REFERENCE 1 (bases 1 to 927) TITLE Full-length cDNA libraries and normalization JOURNAL On May 5, 2003 this sequence version replaced gi:30370217. Contact: Genoscope Genoscope - Centre National de Sequencage	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.ons.fr, Web: www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-Oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and Cloned into the Not I and ECOR V sites of the pCNACSORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODIO36DC10QP1&c=6541.r.	FEATURES Location/Qualifiers 1. 927 forganism="Homo sapiens" /mol_type="mRNA" /db xxef="texaon:9606" /clone="CSODIO36FYEO" /clone lib="Homo sapiens FLACENTA COT 25-NORMALIZED" /clone lib="Homo sapiens FLACENTA COT 25-NORMALIZED" /clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /clone lib="Homo sapiens Primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECOR V	ORIGIN Alignment Scores: 3.6e-146 Length: 927 Score: 1446.50 Matches: 271
TITLE Full-length cDNA libraries and normalization Unpublished Contact: Feng Liang Email: fliang@lifetech.com URL: Contact: Feng Liang Email: fliang@lifetech.com URL: REPERENCE 2 (bases 1 to 1759) AUTHORS AUTHORS Genoscope. JOURNAL By 19 1006 ENEX cedex - FRANCE (E-mail: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr: Web:	Alignment Scores: 5.25e-147 Length: 1759 Pred. No.: 1458.00 Matches: 278 Score: 1458.00 Matches: 278 Percent Similarity: 88.82\$ Conservative: 0 Best Local Similarity: 88.82\$ Mismatches: 2 Query Match: 3 Gaps: 1	-10-689-742-160 (1-280) x CR598502 (1-1759) 1 MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet	121 AGTAGAGTGGCACCATCACTGCAGCCTTGACCTCCCTGGCTCAGGAAICCTC 36	Oy 68 LeuGlyLeuLeuPhePheGlnTyrTyrGlnLeuSerAanThrGlyGlnAspThrIBSer 87	Oy 128 LysaladlyalaHisArgCysSerProCysThrGluGlnTrpLysTrpHisGlyAspAsn 147

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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr. Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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        Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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  Bukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Butheria; Primates; Catarrhini; Hon
1 (bases 1 to 914)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDNA libraries and normalization
Unpublished (2001)
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BX391810.1 GI:30615587
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Mismatches:
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Homo sapiens
97.84%
97.48%
95.92%
Percent Similarity:
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sapiens (human)
sapiens
99.28%
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95.39%
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Percent Similarity:
Best Local Similarity
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I (bases 1 to 1049)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30545374.

Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand CDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                  AL541315

AL541315 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE006YK19 5-PRIME, mRNA sequence.

AL541315

AL541315.3 GI:45716909
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cloned
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                                                                                                                                                                                  231 ProArgSerArgAspCysValAlaIleLeuAsnGlyMetIlePheSerLysAspCysLys 250
                                                                                                                              TrpMetAspGlyThrProPheThrSerGluLeuPheHisIleIleIleAspValThrSer 230
                                                                                                                                                                                                                                      GluLeuLysArgCysValCysGluArgArgAlaGlyMetValLysProGluSerLeuHis
                                                                                                                                                                                                                                                     GAATTGAAGCGTTGTGTGTGTGAGAGAAGAAGGCAGGAATGGTGAAGCCGAGAGAGCCTCCAT
                                       ACCATGCTGAAGATAAACAAACAAGAAGACCTGGAATTTGCCGCGTCTCAGAGCTACTCT
                                                                            GluPhePheTyrSerTyrTrpThrGlyLeuLeuArgProAspSerGlyLysAlaTrpLeu
                                                                                                                                                 TGGATGGATGGAACCCCTTTCACTTCTGAACTGTTCCATATTATAATAGATGTCACCAGC
                                                                                                                                                                                                           CCAAGAAGCAGAGACTGTGTGGCCATCCTTAATGGGATGATCTTCTCAAAGGACTGCAAA
 TICTATAAAGACAGCAAAAGTIGGGAGGACIGTAAATAITITCIGCCTIAGIGAAAACTCT
                         ThrMetLeuLys1leAsnLysGlnGluAspLeuGluPheAlaAlaSerGlnSerTyrSer
                                                                                                      GAGTITITICIACITITICGACAGGGCTITITIGCGCCCTGACAGTGGCAAGGCCTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence belongs to sequence cluster 6541.r
For more information about this cluster, see
http://www.genoscope.cms.fr/cdna?e=CSODE006AF10QP1&c=6541.r.
_Location/Qualifiers
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Pred. No.:
Score:
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BX324788 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA CCI 25-NORMALIZED Homo sapiens CDNA BX324788
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                                                                                                                                                                                            AAGTACAGCACGACGACGACGATGGTGATGATGGGGGACACCACCATGAGCCTGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 GGGCTGGCAGCCCTGGGGCTTTTGTTTTTCAGTACTACCAGCTCTCCAATACTGGTCAA
                                                                                                                                                       LysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMetSerLeuHis
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Conservative:
Mismatches:
Indels:
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30617945.
Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
z rue Gaston Cremieux, CP 5706 - 91057 EWRY cedex - FRANCE
Email: seqrefégenoscope. Cns.fr. Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dI) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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958 bp mRNA linear EST 29-APR-2004
S199696 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
CLONE CSODIO81YG24 5-PRIME, mRNA sequence.
BX399696
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lst strand cDNA was primed with a NotI-oligo(dT)
primer. Five end end entiched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
                                                                                                                               LeuGluPheAlaAlaSerGlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeu
                                                                                                                                                          585 CTGGAATTTGCCGCGTCTCAGAGCTACTCTGAGTTTTTTCTACTCTTATTGGACAGGGCTT
                                                                                                                                                                                                                         LeudrgProdapSerGlyLysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGlu
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                                                                                                                                                                                                                                                                                                                                                                                                      241 AsnGlyMetIlePheSerLysAspCysLysGluLeuLysArgCysValCysGluArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                              TGGAAATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGAC
                                              161 CyslysTyrPheCysLeuSerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAsp
                                                                       705 CIGITCCATATIATAATAGATGICACCAGCCCAAGAAGCAGAGACTGIGIGGCCATCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261 AlaGlyMetValLysProGluSerLeuHisValProProGluThrLeuGlyGlu 278
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Matches:
Conservative:
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1422.50
98.53$
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             Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

E 1 (bases 1 to 1001)

Li,w.B., Gruber.C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

On May 2, 2003 this sequence version replaced gi:30336406.

On May 2, 2003 this sequence version replaced gi:30336406.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the privyEpoRT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue type="PLACENTA COT 25-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR vites of the pCMVSPORT 6 vector. Library was normalized.
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone="CSODI049YB09"
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AUTHORS
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On May 1, 2003 this sequence version replaced gi:30310588.

Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Ist strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1076)
11, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length, Charl libraries and normalization
Unpublished (2001)
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Conservative:
Mismatches:
Indels:
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                                              57 ATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATGGGGACACACCATG
                                                                                                                                                                                            117 AGCCTGCATTCTCAAGCCTCTGCCACAACTCGGCATCCAGAGCCCCGGCGCACAGAGCAC
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1. (bases 1 to 964)

2. (bases 1 to 964)

3. Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

L. Unpublished (2001)

On May 2, 2003 this sequence version replaced gi:30335767.

Contact: Genoscope

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                       BX339075

964 bp mRNA linear EST 07-APR-2004
BX319075 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI067YK14 5-PRIME, mRNA sequence.
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//do xref="taxon:9606"
/db xref="taxon:9606"
/clone="CSODIO67YK14"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tis strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized.
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                                                                                                                                                                                  LysAlaTrpLeuTrpMetAspGlyThrProPheThrSerGluLeuPheHisIleIleIle
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             AsnCysTyrGlnPheTyrLysAspSerLysSerTrpGluAspCysLysTPheCysLeu
                                                                   SerGluAsnSerThrMetLeuLysIleAsnLysGlnGluAspLeuGluPheAlaAlaSer
                                                                                   CAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGCTTTTTGCGCCCTGACAGGGC
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180 GGATCCTGGTTCCAAGTTTTTCAGTACTACCAGCTCCCAATACTGGTCAAGACACACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580 AGTGAAAACTCTACCATGCTGAAGATAAACAAACAAAGAAGACCTGGAATTTGCCGCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AspValThrSerProArgSerArgAspCysValAlaIleLeuAsnGlyMetIlePheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 LysAspCysLysGluLeuLysArgCysValCysGluArgArgAlaGlyMetValLysPro
                                                                                                                             MetGlnAlaLysTyrSerSerThrArgAspMetLeuAspAspAspGlyAspThrThrMet
                                                                                                                                                                                     SerLeuHisSerGlnAlaSerAlaThrThrArgHisProGluProArgArgThrGluHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAATATTTCTGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnSerTyrSerGluPhePheTyrSerTyrTrpThrGlyLeuLeuArgProAspSerGly
 964
265
0
6
6
2
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                  (1-964)
```